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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength	DB	ID	Description
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ALIGNMENTS

	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS		KEYWORDS SOURCE	ACCESSION VERSION	RESULT 1 BQ853899/c LOCUS DEFINITION
Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]	http://compgenomics.ucdavis.edu/ Unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore]	Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project	Lactuca. 1 (bases 1 to 129) Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;	EST. Lactuca sativa. Lactuca sativa.	QGB21M16, mRNA sequence. BQ853899 BQ853899.1 GI:22239364	BQ853899 129 bp mRNA linear EST 14-AUG-2002 QGB21M16.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone

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              Submitted (17 JUN-2002) Weisshaar B., Max-Planck-Institut fuer Junechtungsforschung, Cari-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F23H6. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 TGGCGCCGTTGCCAATTG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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for flanking sequence
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http://www.mpiz-koeln.mpg.de/GABI-Kat/
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                                                                                                                                                                                                                                                      ,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
lanking sequence tag based reverse genetics
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TAG_LIB-QG_ABCDI lettuce salinas
TAG_TISSUE-chemical induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
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from 10 different sources of RNA from a single genotype.
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/cultivar="Salinas"
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http://www.mpiz-koeln.mpg.de/GABI-Kat/.
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                                                                                                                                                                                                                                                                                                                                                                     Li,r., Rosso,M., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Weisshaar, B.
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/clone="GK-118B03-012518"
                      /strain="Columbia 0"
/db_xref="taxon:3702"
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/db_xref="taxon:3702"
                                                                              /organism="Arabidopsis thaliana
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines" /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from

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RESULT 5
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BH243164 199 bp I
AUIHC32TR AUIH Arabidopsis thaliana
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For addtional information, see http://www.tigr.org/tdb/at/at.html
Seq primer: TF
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llarity 100.0%;
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larity 100.0%;
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sheared to 0.9-1 Kbp before
a 26 c 30 g 73 t
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/db_xref="taxon:3702"
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/note="Organ: Leaf
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                                                                                                      Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                   Arabidopsis thaliana.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 216)
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Arabidopsis thaliana genome survey sequence T7 end of BAC T3D23
TAMU library from strain Columbia of Arabidopsis thaliana, genom
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18; Conser
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Town, C.D., Whitelaw, C.A., Pai, G., Van Aken, S.E., Utterback, T.V., Feldblyum, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC F1307
Unpublished (2001)
                                                                                                                                                                Genoscope.
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chris Town
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                                                                                                                                                                                              Unpublished
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From Wash. U contig 1003.
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/strain="columbia"
/db_xref="taxon:3702"
/clone="AUIHC32"
/clone_lib="AUIH"
/note="Vector: pHOS2; Site_l: Bstx
DNA inserted into pHOS2 using Bstx
DNA inserted 34 g 68 t
                                                                    www.genoscope.cns.fr)
Location/Qualifiers
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                        136 TGGCGCCGTTGCCAATTG
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                                                              T22F21TF TAMU
thale cress
                           B62585.1 GI:2629347
                                        sequence.
B62585
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BH243803
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Town,C.D., Whitelaw,C.A., Pai,G., Van Aken,S.E., Utterback,T.V., Feldblyum,T.V. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; II; Brassicales; Brassicaceae; Arabidopsis.
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AUIRB17TR AUIR Arabidopsis th
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/clone_lib="TAMU"
/note="end : T7"
a 40 c 40 g
                                                                                                     FAOM
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/note="Yector: pHOS2; Site_1: BstXI; 2-3 kb sheared
DNA inserted into pHOS2 using BstXI linkers"
45 c 48 g 109 t
                                                                                                                                                                                                                                                                                                   /db_xref="taxon:3702"
/clone="AUIRB17"
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/strain="Columbia"
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Pred. No. 1.1e+02;
; Mismatches 0;
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Pred. No.
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c clone
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T22F21, DNA
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AUIRB17, DNA
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RESULT 9
BH244138
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Best Local :
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source
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                                                                                                                                                            1 (bases 1 to 401)
Town,C.D., Whitelaw,C.A., Pai,G., Van Aken
Feldblyum,T.V. and Fraser,C.M.
Survey sequencing of Arabidopsis thaliana
Unpublished (2001)
Other_GSSS: AUIMA26TR
Contact: Chris Town
                                                                                                                                                                                                                                                                          Arabidopsis thaliana.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Spermatophyta; Magnollophyta; Enassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BH244138
                             Class: sheared ends
                                                           Email: cdtown@tigr.org
From Wash. U contig 1440.
                                                                                              9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                  401
AUIWA26TF AUIW Arabidopsis the
sequence.
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                                                From Wash. U contig
Seq primer: TF
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Seq primer: M13-21
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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Unpublished (1997)
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                                               primer:
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301 838 0208
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Location/Qualifiers
          Location/Qualifiers
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/note-"Vector: BeloBACII;
; Produced by Rod Wing"
71 c 77 g 97
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|strain="Columbia"
|/db_xref="taxon:3702"
|/clone="T22F21"
|/clone=lib="TAMU"
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Pred. No. 1.3e+02;
; Mismatches 0;
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                                                                                                                               Rockville,
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c clone
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AUIWA26, DNA
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RESULT 11
BH243289
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Best Local
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                                                                                                   302
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sequence.
BH243289
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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                       BH243289
AUIHF63TR AUIH
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                                                                                                                                                                                                                                                                                                                                           Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                Email: cdtown@tigr.org
From Wash. U contig 1440.
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larity 100.0%;
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/note="Vector: pHOS2; Site_1: BstXI; 2-3 kb sheared
DNA inserted into pHOS2 using BstXI linkers"
70 c 93 g 122 t
                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/strain="Columbia"
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/clone="AUIWA38"
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/clone="AUIWA26"
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/strain="Columbia"
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                     415 bp DNA linear GSS 13-
Arabidopsis thaliana genomic clone AUIHF63,
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Arabidopsis thaliana
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Pred. No.
                                                                                                                                                Score 18; DB 17;
Pred. No. 1.3e+02;
; Mismatches 0;
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1.3e+02;
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                                                                                                                                                                         Length 410;
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clone AUIWA38, DNA
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BH243156/c
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sequence.
BH243156
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                                                                                                                                                      9712 Medical Center Drive, Tel: 301-838-3523
                                                                                                                                                                                                          Unpublished (2001)
Other_GSSs: AUIHC93TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                       Town.C.D., Whitelaw,C.A., Pai,G., Van Aken,S.E., Utterback,T.V., Feldblyum,T.V. and Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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Town, C.D., Whitelaw, C.A., Pai, G., Van Aken, S.E., Utterback, T.V.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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GSS.
                                                                                          Email: cdtown@tigr.org
From Wash. U contig 10
                                                                                                                                                                                                                                                                     Survey sequencing of Arabidopsis
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From Wash. U contig 1003
                                                                                                                                    Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
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                    Location/Qualifiers
1. .418
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|stratin="Columbia"
|/db_xref="rtaxon:3702"
|/clone="AUIHF63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="AUIH"
/note="Vector: pHOS2; Site_1:
/note="Vector: pHOS2; Site_1:
DNA inserted into pHOS2 using
DNA 99 c 81 g 119 t
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:16918936
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                                                                                                                                                                        MD 20850, USA
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BH252783
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                                                                                       Query Match
Best Local
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 209
                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALK_013862 Arabidopsis thaliana TDNA linear GSS 28-NOV-200 thaliana genomic clone SALK_013862, DNA sequence.

BH252783
                                                                                                                                                                                                                                                                                                                                                                                                                    Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis Genome Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                    TGGCGCCGTTGCCAATTG 18
 TGGCGCCGTTGCCAATTG
                                                                                                                                                                 105
                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ecker@salk.edu
                                                                                                                                                    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 99 c 69 g 146 t
                                                                                                                                                                                                                                                                                                            /clone="SALK_013862"
                                                                                                                                                                                                                                                                                                                         /strain="Columbia 0"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/strain="Columbia 0"
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/db_xref="taxon:3702"
/db_xref="taxon:3702"
/clone="AUTHC93"
/clone=11b="AUTH"
/note="Vector: pHoS2; Site_1: BstXI; 2-3 kb sheared BAC
DNA inserted into pHOS2 using BstXI linkers"
a 82 c 94 g 90 t
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                                                                                     100.0%;
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226
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                                                                Score 18; DB 17;
Pred. No. 1.3e+02;
Mismatches 0;
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Pred. No. 1.3e+02;
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                                                                                                    Length 419;
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Prednis, L., Shinn,
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ORGANISM
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VERSION
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DEFINITION
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BH244105/c
                                                                                                                              TITLE
                                                                                                                                                             AUTHORS
                                                                                                        JOURNAL
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Best Local :
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9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                 sequence.
BH244079
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                                                                                        Survey sequencing of Arabidopsis thaliana BAC F9022 Unpublished (2001) Other_GSSs: AUIRB53TF
                                                                                                                                     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 424)
Town,C.D., Whitelaw,C.A., Pai,G., Van Aken,S:E., Utterback,T.V.,
Feidblyum,T.V., and Fraser,C.M.
                                                                        Contact: Chris Town
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AUIRB53TR AUIR Arabidopsis tl
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18; Conserv
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Survey sequencing of Arabidopsis thaliana BAC F13C23
Unpublished (2001)
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AUIWA21TR AUIW Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="AUIW"
/note="Vector: pHOS2; Site_1: BstXI; 2-3 kb sheared
DNA inserted into pHOS2 using BstXI linkers"
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/strain="Columbia"
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/clone="AUIWA21"
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AUTHORS	RESULT 1 AB073161/c LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM		C C C C 4 4 2 2 4 4 4 4 5 4 4 4 5 4 4 5 6 6 6 6 6 6 6 6	00 39 40 40	c 36	C C 33		322 3098	c 26 27		c 21 c 22		c 16		c 12		ഗ ക ∙	C 7 6 6		ი ი "ას —	Result No. S
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i,T., Tsuruoka,H. a	3539 bp DNA li Iliana DNA, chromosome 4 centro 18149201 Iliana (cultivar:Columbia) DNA, Iliana diplantae; Streptophyta; Embry Magnoliophyta; eudicotyledons; ds II; Brassicales; Brassicace	ALIGNMENTS	T17A2 AC009529 AB062093 AP002067	AB024037 AB062087	AC016828 AB026642	T5H22 AC068901	T10118 T15F17	AB046427 AC067965 F14C23	AB046430 AC090030	AB046428 AB046428	AC090029 T6L9 AC007209	755	AX059474 AX059474 AX059513					050	C109	AB073161 AC093090 T9F19	
and Kotani,H.	linear PLN 26-FEB-2002 centromere region, BAC a) DNA, clone:T5110. Embryophyta; Tracheophyta; ledons; core eudicots; sicaceae; Arabidopsis.		AF160183 Arabidops AC009529 Arabidops AB002093 Arabidops AB002067 Arabidops	Arab		Arak			Arak Arak				AX059474 Sequence AX059513 Sequence			Sequenc			Arak	ABU/3161 Arabidops ACO93090 Arabidops AF104920 Arabidops	cription

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                              Submitted (31-AUG-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org Address all correspondence to:at@tigr.org
                                                                                                       Direct Submission
Submitted (09-AUG-2001) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org
3 (bases 1 to 18433)
Town, C.D., and Kaul, S.
                                                                                                                                                                                                      Town,
                                                                                                                                                                                                                                 Town,C.D., Haas,B.J., Wu,D., Maiti,R., Hannick,L.I., Chan,A.P., Tallon,L.J., Rooney,T., Utterback,T.R., Vanaken,S.E., Feldblyum,T.V., White,O. and Fraser,C.M.
Arabidopsis thaliana chromosome 3 BAC F1C23 genomic sequence Unpublished
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                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II, Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 18433)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 3539) . Kotani, H. and Kumekawa, N. Direct Submission
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and annotation"
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/note="overlap to BAC F8H12,
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/cultivar="Columbia"
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/clone="T5I10"
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                                             Tracheophyta;
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Strowmatt,C., Johnson,D. and Le,T.
The sequence of A. thaliana T9E19
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The 5' clone is T2L5, 200 bp overlap; 3' clone is F7N22, 200 bp overlap. Actual start of this clone could not be found, the first known base of overlap is at 36622 of T2L5; actual end is at 76001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence from more than one subclone
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/evidence=not_experimental
/protein_id="AAC72876.1"
/protein_id="AAC72876.1"
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/translation="MAYSKPEYISDIENVLKGKPEMOFLLDSPFGELFKIPONKASF
/Kranslation="MAYSKPEYISDIENVLKGKPEMOFLLDSPFGELFKIPONKASF
NAKLVLGLICRQLVTKKVNEMMIVFGGHPIRFGLREFSILTGLECGKYPKKKDVDDVI
NVKPECESVMNTLFDERFGDTVPTIADLVSWLDEEESMEGWGQLASLIIIVDGVVAA
HSNPNRFTSKTVEMMKNLKEFCKYPMGRVSFTRTLGRIANFQTPYDAQQLIRDLYGS
YALHGFPLALQLLAFETIPSIAKLGPDDVLNRTFAERSHRLASLEAIRTSRILECEA
ADEVEVNYIVKPADNVCPPSLSWDDEYDDPRVDYIEALLIDGHQMQEDEWVGGYARVP
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St. Louis, MO 63108, USA
e-mail: rwilson@watson.wu
                                                                                                                                                                                                                                  /gene="T9E19.2"
join(57. .893,969.
/gene="T9E19.2"
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/cultivar="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                   Submitted (08-FEB-2002) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, odtown@tigr.or.

* NOTE: This is a 'working draft' sequence. It currently 'consists of 7 contigs. The true order of the pieces 's is not known and their order in this sequence record is 'arbitrary. Gaps between the contigs are represented as 's arbitrary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Town,C.D., Haas,B., Tallon,L.J., Rooney,T., Ciecko,A., Utterback,T., Vanaken,S., Feldblyum,T., White,O. and Fraser,C.M. Arabidopsis thaliana 'IGF' BAC 'F9022' genomic sequence near marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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This record will be updated with the finished sequence
as soon as it is available and the accession number will
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vn,C.D., White,O. and Fraser,C.M.
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GESKLVTGMEVEIPEKTHSDPPSPFQVVNNVIRELDTKAVGDLAAATDVEELRILTQG
QTHLLTKRVGDFKKCFNKNGFKWGKLLSDIANGVHINREPNMKWLKDVDVVYAPMNWK
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APVTGKRSFKELEDOMYOMHEDMKDFVRDQIRALSYGCUSKEEDLDVPGVHTTA
VEGRRRFSKPKKUNYERAUTTELDSUNKEDMGDFIDEODRGNVVVCKTYPLGSMSGTV
YVTQEERPVEEATVDTEMEEVPSNESARVSEVDLLDNGPKDVAEPGLVGTHTGADEIA
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/gene="T9E19.1"
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/gene="T9E19
  yap of unknown 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 33329)
Town,C.D. and Kaul,S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-MAR-2000) The Institute for Genomic Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E., Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C., Fraser,C.M. and Venter,J.C.
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1 (bases 1 to 33329)
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                                                                                 /note="2721 nt before this point were not included in the submitted sequence, due to overlap with another BAC" complement(383. 431) /rpt_family="AT_rich" complement(2109. 2135) /rpt_family="AT_rich" /rpt_family="AT_rich"
                                               complement(2211. .2267)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                  complement(1. .482)
rpt_family="AT_rich"
                                                                                                                                                                                                                                                                        /note="overlap with BAC clone F15K19 (AC006429:1. .482)."
                                                                                                                                                                                                                                                                                                                               /map="g4532"
/clone="F16G22"
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                    'chromosome-"2"
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/clone="IGF-F9022"
6125 c 6878 g
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/strain="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AT_rich"
complement(13763, .16746)
/gene="At2g10900"
/note="r*c"
                                                                                                                                                                                                                                                                                        /note="F16622.4; similar to GB:AAA75253; some members of this protein family have a weak CCHC zinc fingers that is mostly from retroviral gag proteins (nucleocapsid) complement(join<13763. .14997,15212. .15445,15881. .1608
  complement(join(13763. 16536. .16746))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(11206. .11773)
//gene="At2g10910".
/note="DNA sequence similar to non_LTR retrotransposon
psuedogene for reverse transcriptase GB:L47192"
                                                                               /product="putative Tall-like
/protein_id="AAD28647.1"
/db_xref="GI:4733964"
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7271. .7442
                                                                                                                                                                 codon_start=1
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/note="p1/222
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/protein_id="AAD28646.1"
/db_xref="GI:4733963"
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/rpt_family="AT_rich"
2951. .2992
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/gene="At2g10930"
|oin/K477
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)oin(5423. .56
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Tall-like non-LTR

non-LTR

retroelement protein"

.15445,15881.

.16084,

.16084, Ľ.

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val5. .7085
/note="DNA sequence similar
GB:U76697"
                                                                                                    DLFKIFPQATTYLRQIQKGGGSGCFEFIRGEVCTKDLSQNNTFYFIF*complement(6054. 6076)
                                                                                                                                                /translation="mevsdgssqvlnsmkhvastradedpdetstllsstlldtvpr
LVLVtyCVRVLMLDQYQETIALSQEVmmeDGRREENVPMNCPIPVVKRRMKAPKHVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich"
complement(3184. .3205)
                                                                                                                                                                                                 /product="unknown protein"
/protein_id="AAD28645.1"
/db_xref="GI:4733962"
                                                                                                                                                                                                                                                                                                         join(5472. .5657,5687. .5861,5984. .6072)
∕gene≔"At2g10930"
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22177. .
                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
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/db_xref="GI:4733965"
/translation="MAEYHHHHSLDQSLYHQVEYYNHHPLDQSLYHMVESLIIIHSTS
LLDCQLQSLLHSALNQTLEHKQEKKTPAYHSTIHSTTWVEYRS"
complement(24277. .24387)
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retroelement.#Rf:ATR0033|X81801 Athila retroelement"
22629. .22733
/rpt_family="Rf:gi|895701|emb|X89195.1|ATSATDNA1
A.thaliana DNA of a 180bp satellite
                                                                                                                                                                                                                                       /rpt_family="Rf:106B centromeric repeat x93611, 106B is diverged copy of the Athila retroelement, 300 coples#Rf:gill100798|embly39611.1|A7106B A.thaliana centromeric repeat region (clone 106B)#Rf:ATR0044|x93611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Rf:gi|895701|emb|x89195.1|ATSATDNA1
A.thaliana DNA of a 180bp satellite
junction#Rf:ATR0034|X89195 clone H12 of Athila 180-bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Rf:ATHILA|ATHILA A.thaliana DNA for Athila
retroelement.#Rf:ATR0033|X81801 Athila retroelement"
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MRCPIFGDKGKQSIFKEDPKKDNTLQRYKGAAINGSVPGTSSGSTRAVFAEPSQGLTS
LDKKDASIQDSYNRSKQISGIKAKKGRRNLFPAGES
MGFDDHEKKHLEAFLAPEAGKTVTDLGTLGANMEGILSGTMPSKVVRKKFSGPEEVT
IQNKAENALELAEQHDLFSDDLSQLLAQSSPLEGDPSLQFMDYKMEDKKSSGVELTHE
DGEFFAANEENFDGDKLEVVLLPINTVSEMNVNMVSVSENVPNEQAHEEEMEGKSQGE
                  /gene="At2g10870"
                                                        complement(<25459. .>25710)
/gene="At2g10870"
                                                                                                /rpt_family="Rf:centromeric |
19092 1751nt includes within
complement(25459. .25710)
/gene="At2g10870"
/note="F16G22.7; predicted b)
                                                                                                                                                                                                      complement(25075. .25134)
                                                                                                                                                                                                                         106B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="F16G22.6; similar to hypothetical protein
GB:AAC26673"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Rf:ATHILA|ATHILA A.thaliana DNA for Athila
retroelement.#Rf:ATR0033|X81801 Athila retroelement"
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22349. .22631
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                                                                                                                                                                                                                                                                                                                       /rpt_family="Rt:centromeric report 19092 1751nt includes within it 106B centromeric
                                                                                                                                                                                                                                                                                                                              24643.
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junction#Rf.ATR0034|X89195 clone H12 of Athila 180-bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="At2g10880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="At2g10880"
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                                                                                                                                                              repeat from T7M24 17342 to it 106B centromeric repear
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SOURCE
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AX059500
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23423 TGGCGCCGTTGCCAATTG 23406
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Sequence 233 from Patent WO0055325
AX059500
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                                                                                                                                                                                                                                        thale cress.
Arabidopsis thaliana
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Sequence 194 from Patent WO0055325.
AX059461
                                                                                                            Plant chromosome compositions and methods Patent: WO 0055325-A 233 21-SEP-2000;
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                                                                         University of Chicago (US)
Location/Qualifiers
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
7401 c 7909 g 9799 t
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/db_xref="taxon:3702"
7544 c 7078 g 10298 t
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/protein id="AAD28649.1"
/db_xref="G1:4733966"
/translation="MEFDGGVLALPAVFVAESFVGVEALVSQRLRKRKGKRVRLEEEE
DDEPELGVDANNEEDCGVYGDEDCDAVEDIVGGGENDDN"
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Plant Chromosome compositions and methods
Patent: WO 0055325-A 212 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 39104)
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AX059479
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18; Conserv
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AX059548
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Plant chromosome compositions and methods
Patent: WO 0055325-A 281 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Arab
1 (bases 1 to 38519)
                          TGGCGCCGTTGCCAATTG 7779
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/db_xref="taxon:3702"
7680 c 7833 g 12033 t
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/db_xref="taxon:3702"
7622 c 7434 g 11646 t
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AX059477/c
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AX059497/c
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DEFINITION
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AX059456/c
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AX059477 42
Sequence 210 from Patent
AX059477 GI:12311582
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                                                                                                                                                                   l Similarity
18; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 42112)
Preuss, D., Copenhaver, G. and Keith, K.
Plant chromosome compositions and methods
Patent: WO 0055325-A 230 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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AX059497
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Plant chromosome compositions and methods
Patent: WO 005535-A 189 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (Dases 1 to 40480)
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Similarity 100.0%;
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/db_xref="taxon:3702"
8525 c 8423 g 12287 t
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/db_xref="taxon:3702"
7912 c 8765 g 11297 t 2:
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RESULT 8 AX059548 LOCUS

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Rosidae; to 47383)
Previss D. Corenhaver G. and Keith K.
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          Arabidopsis thaliana Eukaryota; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Aagpoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                18;
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Patent: WO 0055325-A 192 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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Sequence 192 from Patent WO0055325.
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Location/Qualifiers
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185 from Patent W00055325
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/db_xref="taxon:3702"
9919 c 9688 g 13496 + ""
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/db_xref="taxon:3702"
8859 c 8866 g 11961 t
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100.0%; Pred. No. 81;
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Preuss,D., Copenhaver,G. and Keith,K.
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Patent: WO 0055325-A 202 21-SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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/db_xref="taxon:3702"
7963 c 8596 g 15790 t
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10020 c 9567 g 14078 t
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                  Score
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Copyright (c) 1993 - 2003
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Compugen Ltd.
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Plant retroelement
Plant retroelement
BAC containing rep
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WO9960842-A2	Glycine max	Retroelement; soybean; ss.		27-MAR-2000	AAZ35269;	35269		14.8	14.8 14.8	14.8	14.8 14.8	14.8	15	15.4	15.4	15.4	15.4	15.4	15.4	15.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	17	17	₽ F	18	18	18 18
A2.	×		retroelement	0 (firs		standard;		82.2	82.2 82.2	82.2	82. 82. 2	82.2	83.3	85.6	85.6	85. 6	85.6	85.6	85.6	85.6	91.1	91.1	91.1 91 1	91.1	91. 1	91.1	91.1	94.4	94.4	100.0	100.0	100.0	100.0
		retrovirus;	nt primer	st entry)		i; DNA;	•	1089	849 986	573	417 417	345	412 163319	1082138	163319	94895	80450	8778	1713	548 1713	134499	103929	90336	83390	79100	64415	50959	151826	40349	1082138	134499	109973	96583 96988
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		transgenic plant; gene	binding site version			Ρ.	ALIGNMENTS	ABK73473	AAC45687 AAC45686	ABK77414	AAZ53128 AAZ53129	ABN23008	AAA/96/8 AAF22306	AAF22305	AAF22306	AAF22302	AAF22295	ABL29794	AAZ38242	AAA82386 AAT36389	AAF22286	AAF22287	AAF22292	AAF22283	AAF22300	AAF22279	AAF22304	AAF22292	AAF22278	AAF22305	AAF22286	N	AAF22297 AAF22290
		ne transfer; primer;	•					lichenif	Arabidopsis thalia Arabidopsis thalia	213	Neisseria meningit Neisseria meningit	Human ORFX polynuc	Pinus radiata celi Arabidopsis thalia	Arabidopsis thalia	bidopsis tha	BAC containing rep	containing	Drosophila melanog	Vibrio furnissii e	N. meningitidis pa Arvl Beta-N-acetyl	containing	BAC containing rep		BAC containing rep	Containing	BAC containing rep	ъ	BAC containing rep	containin	Arabidopsis thalia	containing	BAC containing rep	BAC containing rep

PA XXX PA XXX PA PA PA XXX PA PA PA XXX PA XXX PA PA XXX PA PA XXX PA XXX PA 29-MAY-1998; 28-MAY-1999; (WRIG/) WRIGHT D A. (VOYT/) VOYTAS D F. 28-MAY-1999; 02-DEC-1999. W09960842-7.0 98US-0087125 99US-0087125 99WO-US11858

Wright DA, Voytas

WPI; 2000-105586/09.

C containing rep C containing rep

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AAF22288 AAF22302 AAF22282

New nucleic acid molecules for imparting agronomically significant

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RESULT 2
AAZ35270
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Best Local
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         This oligonucleotide represents plant retroelement primer binding site A of the invention. The invention provides molecular tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the
                                                                               Disclosure; Page 115; 118pp; English.
                                                                                                        New nucleic acid molecules for imparting characters to plants, especially soybean
                                                                                                                                                                                                                                              29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  env sequences is used to enable transfer of a secondary construct which carries an agronomically-significant characteristic and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that are used to transfer the nucleic acids into plant cells.
                                                                                                                                                                             Wright DA,
                                                                                                                                                                                                                                                                                      28-MAY-1999;
                                                                                                                                                                                                                                                                                                                 02-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                        Retroelement;
    retroelements
                                                                                                                                                                                                     (WRIG/) WRIGHT D
(VOYT/) VOYTAS D
                                                                                                                                                                                                                                                                                                                                          WO9960842-A2
                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                            primer binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ35270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ35270 standard; DNA; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic. In a preferred method, a helper cell line which expresses gag, pol and
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This oligonucleotide represents a soybean retroelement primer binding site (version 1). The invention provides molecular to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characters to
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                                                                                                                                                                            Voytas DF
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 2 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
    into
                                                                                                                                                                                                                                                                                                                                                                                                     retrovirus; transgenic plant; gene transfer;
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99US-0087125.
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                                                                                                                                                                                                                                                                                                                                                                                             site;
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Pred. No. 8
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retroelement carries
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RESULT 3
AAF22281/C
ID AAF22281 standard; DNA; 59590
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                                                                                                                                                                                                                                                        01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                        The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for
                                                                                                                              Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which carries an agronomically-significant characteristic and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase
  Sequence
                                   the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clott.
                                                                                                          Claim 102; Page 351-364; 1449pp; English.
                                                                                                                                                                                  WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                             17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                           Centromere; michrosome; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC containing
                                                                                                                                                                                                                                 (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                      18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at least 1 agronomically-significant characteristic. In a preferred method, a helper cell line which expresses gag, env sequences is used to enable transfer of a secondary which carries an agronomically-significant characteristic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oviral particles that plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 TGGCGCCGTTGCCAATTG
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   59590
                         cytokines,
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99US-0127409.
99US-0134770.
99US-0153584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see AAZ35254-61). Also provi
 17614 A;
                        antibodies, and
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12031 C; 13575 G;
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Pred. No.
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                      factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  #4
 16118 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
 252 other,
                                                                                                                                           useful for
s vectors for
                                   clotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Query Match Best Local Matches

Similarity

100.0%;

.0%;

Conservative

0

Score 18; DB Pred. No. 12; Mismatches

DB 12;

21;

Length 59590;

0

0,

Gaps

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RESULT 5
AAF22283/c
ID AAF22283 S
XX
AC AAF22283;
XY
DT 20-MAR-200
XX
XX
E BAC contai
XX
Centromere
                                                                                                                                    밁
                                                                                                                                                        δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
AAF22279/c
                                                                                                                                                                                                Query Match
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                   The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct comprising a plant centromere, useful producing stably inherited michrosomes which can serve as vector the construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC
Centromere; michrosome; vector; ds.
                                         20-MAR-2001
                                                                                                                                                                                                                       Sequence 64415
                                                                                                                                                                                                                                                                                                                Claim 102; Page 321-335; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Preuss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200055325-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centromere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF22279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF22279 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCH-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-2000;
                                                                                                                                                                                        Local
                                                                                                                                     35451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35456
                   containing repeats from centromeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containing repeats from centromeres
                                                                                                                                                                                                                                                                                                                                                                                2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                          L
                                                                                                                                                                             . Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                         cytokines, antibodies, and growth factors.
                                                                                                                                    TGGCGCCGTTGCCAATTG 35434
                                                                                                                                                         TGGCGCCGTTGCCAATTG 18
                                                                                                                                                                                                                                                                                                                                                                                                  Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            michrosome;
                                                                                                                                                                             100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                        CHICAGO.
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                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0125219.
99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                                                                                                                                     BP; 18698 A; 13554 C;
                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                   <u>ه</u>
                                                                                  83390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector;
                                                                                                                                                                                                                                                                                                                                                                                                    Keith
                                                                                                                                                                             0;
                                                                                                                                                                           Score 18; DB
Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                     13083 G; 18980 T;
                                                                                                                                                                                                 DB
                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #2
                                                                                                                                                                             0;
                                                                                                                                                                                               Length 64415;
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                        as vectors for
                                                                                                                                                                                                                      100 other;
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                                                                                                                                                                             Gaps
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RESULT 6
AAF22289/c
ID AAF22289 standard;
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                  Matches
                         18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                           BAC
                                                                                                                                                                                                                                                                                                                                                                                                                             (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 102; Page 386-404; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
       (UYCH-) UNIV
                                                                                       17-MAR-2000;
                                                                                                            21-SEP-2000
                                                                                                                                WO200055325-A2
                                                                                                                                                  Arabidopsis
                                                                                                                                                                       Centromere;
                                                                                                                                                                                                               20-MAR-2001
                                                                                                                                                                                                                                    AAF22289;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCH-) UNIV CHICAGO.
                                                                                                                                                                                                                                                                                                         71262 TGGCGCCGTTGCCAATTG 71245
                                                                                                                                                                                          containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                              TGGCGCCGTTGCCAATTG 18
                                                                                                                                                                                                                                                                                                                                                                                        83390 BP;
                                                                                                                                                                                                                                                                                                                                                                                                           cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                      proteins such as hormones, enzymes, interleukins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copenhaver
                                                                                                                                                  thaliana
                                                                                                                                                                        michrosome;
                                                                                                                                                                                                                                                                                                                                                  Conservative
        CHICAGO
                                                                                       2000WO-US07392
                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,000WO-US07392
                         99US-0125219.
99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                                                                                                          repeats
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                                                                                                                                                                                                                                                                                                                                                                                        24664 A; 17305 C;
                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                           from centromeres
                                                                                                                                                                        vector;
                                                                                                                                                                                                                                                       90336
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                        17224 G;
                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                        24140 T; 57 other
                                                                                                                                                                                                                                                                                                                                                                    Length 83390;
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                                                                                                                                                                                                                                                                                                                                                                                                                      clotting
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                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Loc
Matches
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                         The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing.
                                                                                        Claim 102;
                                                                                                        Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve a the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                          BAC
                                                                                                                                                                                                    (UYCH-)
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                                                                                                                                                                                                                                                                                                                 21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                   Centromere; michrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF22288 standard; DNA;
          factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors fithe construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 90336 BP; 26524 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selected proteins such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                producing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to a recombinant DNA construct of a pla abidopsis thaliana) centromere. The constructs are useful for ducing stably inherited michrosomes which can serve as vectors for construction of transgenic plant and animal cells expressing ected proteins such as hormones, enzymes, interleukins, clotting transfer and animal cells expressing extensions.
                                                                                                                                                                                                                                                                                                                                                                                                         containing
                                                                                                                                                          2000-587529/55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                     UNIV CHICAGO
          cytokines,
                      proteins such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCGCCGTTGCCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCGCCGTTGCCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokines, antibodies, and growth factors.
                                                                                     Page
                                                                                                                                                                               Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 529-549; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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                                                                                        508-529;
        antibodies, and
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                                                                                                                                                                                                                                                                                                                                                                                   vector;
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                                                                                    1449pp;
                  hormones,
                                                                                                                                                                               Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18837 C;
                                                                                                                                                                                                                                                                                                                                                                                                         centromeres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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Pred. No.
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                                                                                   English.
        growth
                    enzymes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18625
                                                                                                                                                                                                                                                                                                                                                                                                         1-4 #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВВ
          factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                  interleukins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                              2
                                                                                                                                useful
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                                                                                                                      vectors
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RESULT 9
AAF22282/
ID AAF2

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standard;

DNA;

95223

ВP

38265

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AAF22282; AAF22282

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                                                                               RESULT 8
AAF22302/c
AAF22302 standard;
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                                                Query Match
Best Local :
                                        Matches
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Matches
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                         The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromerre. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
                                                                                                                                                                                        Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve a the construction of transgenic plant and animal cells -
                                                                              Sequence 94895 BP;
                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                     Claim 102; Page 804-819; 1449pp; English.
                                                                                                                                                                                                                                                       Preuss
                                                                                                                                                                                                                                                                                                                                                        17-MAR-2000;
                                                                                                  factors,
                                                                                                                                                                                                                                                                          (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                       Centromere; michrosome; vector; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF22302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 92584 BP; 27840 A; 18113 C; 19835 G; 26796 T; 0 other
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 38282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31015
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                   1 TGGCGCCGTTGCCAATTG
                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conserv
                                                 Similarity
TGGCGCCGTTGCCAATTG
                                                                                                  cytokines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCGCCGTTGCCAATTG
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                                        Conservative
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                                                                                                                                                                                                                                                                                             99US-0125219.
99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeats
                                                                             28943 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 94895
                                                100.0%;
                                                                                                  antibodies, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                      0;
                                                                              18101 C; 18466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                Score 18;
Pred. No.
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Pred. No.
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                                       Mismatches
                                                                                                                                                                                                                                                      ζ.
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                                                                                                growth factors.
                                              DВ
12;
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                                                                              G;
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                                                                             29385 т;
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                                                         Length 94895;
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                                      Indels
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                                                                              0 other;
                                                                                                                                                                                                  as vectors
                                                                                                                                                                                                             useful for
                                      0; Gaps
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20-MAR-2001

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RESULT 10

AAF22297/c

ID AAF22297;

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AC AAF22297;

XZ

DE BAC containing repeats from the containing repeats f
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Best Local
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA construct comprising a plant centromere, useful producing stably inherited michrosomes which can serve as vector the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preuss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1999;
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCGCCGTTGCCAATTG 55819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95223 BP; 27974 A; 19452 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 364-385; 1449pp; English.
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                                                                                                 2000WO-US07392
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    99US-0125219.
99US-0127409.
99US-0134770.
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99US-0127409.
99US-0134770.
99US-0153584.
                                                                                                                                                                                                                                                                                                                                     repeats from centromeres
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                                                                                                                                                                                                                                                                                       vector; ds
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Pred. No.
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Matches
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                                                                                                                                                                18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                   Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors futhe construction of transgenic plant and animal cells -
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                              Claim 102;
                                                                                                 WPI;
                                                                                                                      Preuss
                                                                                                                                           (UYCH-) UNIV
                                                                                                                                                                                                                                   17-MAR-2000;
                                                                                                                                                                                                                                                          21-SEP-2000
                                                                                                                                                                                                                                                                               WO200055325-A2
                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                           Centromere; michrosome; vector; ds
                                                                                                                                                                                                                                                                                                                                                 BAC containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 102; Page 716-738; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
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17-SEP-1999;
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                                                                                                                      Copenhaver
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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99US-0154603.
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                                                                                                                                                                                                                                                                                                                                                 from centromeres
                              1449pp;
                                                                                                                      Keith K;
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Pred. No.
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The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for

plant

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RESULT 12
AAF22298
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Best Local S
Matches 18
                                                                                                                                     Query Match
Best Local :
                                                                                                              Matches
                                                                                                                                                                                                                                                                                                 The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of
                                                                                                                                                                                                                         Sequence 109973 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 102; Page 738-763; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells -
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18-MAY-1999;
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the construction of transgenic plant and animal cells expressing
selected proteins such as hormones, enzymes, interleukins, clotting
factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                ractors,
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  5453
                                                                                                           l Similarity
18; Conser
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                            TGGCGCCGTTGCCAATTG
                                                                                                                                                                                                                                                                             cytokines,
  TGGCGCCGTTGCCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCGCCGTTGCCAATTG 49891
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                                                                                                           Conservative
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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100.0%; F
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5470
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Pred. No.
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                                                                                                        Mismatches
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                                                                                                                                                                                                                      22655 G;
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                                                                                                                                                                                                                      31745 T;
                                                                                                                                                               Length 109973;
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                                                                                                        Gaps
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RESULT

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21-SEP-2000

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AAF22303/c
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                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                                                                         AAF22303;
                                                                                                                                                                 AAF22303 standard;
                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
            WO200055325-A2
                                                              Centromere;
                                                                                      Arabidopsis
                                                                                                                20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 102; Page 453-484; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells
                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                     Sequence 134499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Centromere; michrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC containing repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF22286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF22286 standard; DNA; 134499
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                                                                                                                                                                                                                                89656 TGGCGCCGTTGCCAATTG
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                                                                                                                                                                                                                                                                                   . Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copenhaver
                                                              michrosome;
                                                                                      thaliana chromosome 2 centromere.
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                (first entry)
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99US-0127409.
99US-0134770.
99US-0153584.
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                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                     41565 A;
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                                                                                                                                                                 611590
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                     42577 T;
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17-MAR-2000;

2000WO-US07392

99US-0125219.

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RESULT 15
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                  Centromere; michrosome; vector; ds
                                                                                                                                                                                                                                                                                                         Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                              AAF22305 standard; DNA; 1082138 BP
                                                 WPI; 2000-587529/55
                                                                        Preuss
                                                                                                                                                                                                               21-SEP-2000.
                                                                                                                                                                                                                                      WO200055325-A2.
                                                                                                                                                                                                                                                                                                                                20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                        AAF22305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 611590 BP; 181893 A; 124460 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 45; Page 820-959; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
                                                                                              (UYCH-) UNIV CHICAGO.
                                                                                                                     17-SEP-1999;
                                                                                                                                                                                        17-MAR-2000; 2000WO-US07392.
                                                                                                                                                                                                                                                           Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCH-) UNIV CHICAGO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCGCCGTTGCCAATTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copenhaver
                                                                      Copenhaver
                                                                                                                                                                                                                                                                                                       thaliana chromosome 4 centromere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                   99US-0125219.
99US-0127409.
99US-0134770.
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99US-0154603.
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                                                                       Keith
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Pred. No. 13;
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Best Local
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                                                                                                                                         Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;
                                                                                                                                                                                                                                                                                                   Claim 68; Page 977-1388; 1449pp; English.
                                                                                                                                                                          factors, cytokines, antibodies, and growth factors.
1043856 TGGCGCCGTTGCCAATTG 1043873
                                                                                      Local
                                                                     1 Similarity
18; Conserv
                                  1 TGGCGCCGTTGCCAATTG 18
                                                                 100.0%;
nilarity 100.0%;
Conservative 0
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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        US-09-053-702-1
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US-09-072-596-310
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US-08-920-812-13
US-08-920-812-13
US-08-920-812-13
US-08-920-812-17-13
US-08-920-82-177-13
US-09-103-840A-2
4 US-09-103-840A-1
4 US-09-103-840A-1
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6 US-09-103-840A-1
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7 US-09-103-840A-1
8 US-09-103-840A-1
9 US-09-103-840A-1
0S-08-1191-866D-20
US-08-191-866D-20
US-08-620-4120-132
US-09-556-877-132
US-09-556-877-132
US-09-620-4120-132
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US-09-322-478-36
US:08-386-727-5
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Sequence 1
Sequence 3
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  310, App
313, Appl
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42, Appl
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62, Appl
16, Appl
16, Appl
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16, Appl
170, A
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36, Appli
5, Appli
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1, Appli
38, Appl
GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Woytas, Daniel F.
APPLICANT: Voytas, Daniel F.
ITILE OF INVENTION: Plant Retroelements and Methods Related Thereto FILE REFERENCE: P-1065 ISURF Plant Retroelement CURRENT FILING DATE: 1999-05-28
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 150
TYPE: DNA
ORGANISM: Glycine max
US-09-322-478-36
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US-09-322-478-36
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US/09322478

28 13.8 76.7 1659 1 US-08-548-509-4 Sequence 4, Appli 29 13.8 76.7 3538 4 US-09-336-447A-10 Sequence 10, Appl 30 13.8 76.7 4588 4 US-09-453-702B-26 Sequence 26, Appl 31 13.8 76.7 10684 4 US-09-221-017B-401 Sequence 401, App

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RESULT 3
US-08-386-727-5/c
Sequence 5, Appl
                                                                            RESULT 4
US-08-600-452A-5/c
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; MOLECULE TYPE:
US-08-386-727-5
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                                        Patent No. GENERAL I
                                                                    Sequence
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Best Local Similarity
Matches 18; Conserv
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: HOBBS, ANN S.
REGISTRATION NUMBER: 36,830
REFERENCE/DOCKET NUMBER: 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                          ENGTH:
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                                                                                                                                591 GGCGCGGTTGCCAATTG 575
                                                      5, Application US/08600452A
5, 5985644
                                        INFORMATION:
                                                                                                                                               2 GGCGCCGTTGCCAATTG 18
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ROSEMAN, SAUL
BASSLER, BONNI
KEYHANI, NEMAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                      Conservative
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KEYHANI, NEMAT O.
CHITLARU, EDITH
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              Query Match
Best Local Similarity
Matches 16; Conserve
                                                                                         ; NAME/KEY: CDS
; LOCATION: (225)..(1070)
US-09-053-702-1
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US-09-053-702-1
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                                                                                                                                                                                                 SOFTWARE: PatentIn
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09053702
Patent No. 6229069
GENERAL INFORMATION:
APPLICANT: YAMADA, Shigehiro
                                                                                                                                                                                                                      FILE REFERENCE: 230-122P
CURRENT APPLICATION NUMBER: US/09/053,702
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD FOR CONTROLLING WATER CONTENT OF PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0766
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                ORGANISM: Mesembryanthemum crystallinum
                                                                                                                                                                     LENGTH: 1272
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                      FEATURE:
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COMPUTER READABLE FORM:
"""" TYPE: Floppy disk
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ADDRESSEE: FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHITLARU, EI APPLICANT: ROWE, CHRIS APPLICANT: YU, CHARLES TITLE OF INVENTION: BACK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1713 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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1: CA
PRY: USA
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TGGCGCCGTTGCCAATTG 18
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                              Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                         82.2%;
88.9%;
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                                         Score 14.8;
Pred. No. 56;
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Pred. No. 28;
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                            Mismatches
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                                                         DB
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                                                         4;
                           2;
                                                        Length 1272;
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                            Indels
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                           Gaps
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В

841 TGGCTCCATTGCCAATTG 858

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: LENGTH: 3097
; TYPE: DNA
; ORGANISM: Infectious pancreatic necrosis virus
US-09-282-147-38
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Best Local S
Matches 16
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SEQ ID NO 38
LENGTH: 3097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/282,147
CURRENT FILING DATE: 1999-03-31
EARLIER APPLICATION NUMBER: US/60/080,278
EARLIER FILING DATE: 1998-03-31
EARLIER APPLICATION NUMBER: PCT/US97/12955
EARLIER FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS TITLE OF INVENTION: TRANSCRIPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VAKHARIA,
APPLICANT: YAO, Kun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tent No.
                                                                                                                             COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            APPLICANT: Hendricks
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                             ATTORNEY/AGENT INFORMATION:
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                                                               APPLICATION NUMBER: FILING DATE: 05-MA
                                                 CLASSIFICATION:
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REGISTRATION NUMBER:
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Vedvick, Thomas S.
Vedvick, Daniel R.
                                                                                                                                                                                                                                                            6300 Columbia Center,
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Dillon, Davin C.
Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                      HENDII KOON, RONALD C.
HENDION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                          odes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
                                                                                                                                                                                                                                                                                SEED and BERRY LLP
                 David J.
                                                                 05-MAY-1998
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                                                                                US/09/072,596
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Pred. No. 6
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                                                                                                                                                                                                                                                             701 Fifth Avenue
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US-08-920-812-13
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Patent No.
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Best Local S
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                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                           MOLECULE TYPE: (
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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LENGTH: 962 base pairs
                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
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                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                         ORGANISM:
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 29-AUC
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                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
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                                                                         FOPOLOGY:
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15; Conserva
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: nucleic acid
NDEDNESS: single
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                                                                                                    nucleic acid
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            Clinical Isolate P2-2
                                                                                                                  9515 base pairs
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                                                         Genomic DNA
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93.8%;
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Pred. No. 8
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Query Match

80.0%; Score 14.4;

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Length 9515;

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RESULT 10
US-08-921-177-13/c
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US-08-920-827-13/c
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                    Patent No. 5798211 GENERAL INFORMATION:
                                               Sequence 13,
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Pseudomonas aeruginosa
STRAIN: Clinical Isolate P2-2
     APPLICANT:
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TELEFAX: 25-3856
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STREET: GULL
Chicago
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                                                                                                                                                                                            Local
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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REFERENCE/DOCKET NUMBER: 19036/32420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                     515 GCGCCGTTGCCAATCG 500
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15; Conserv
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                                   3, Application US/08921177 
5798211
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                                                                                                                                                                                                                                                                                                                                     nucleic acid
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     Ohno, Tsuneya
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                                                                                                                                                                          Score 14.4; D
Pred. No. 1.1e
0; Mismatches
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US-08-362-577C-13/c
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US-08-921-177-13
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Best Local S
Matches 15
                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                             Sequence 13
                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                 NUMBER OF SEQUENCE ADDRESS:

CORRESPONDENCE ADDRESS:

Marshall, O'Toole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: (ORIGINAL SOURCE:
                    COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                           TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
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NUMBER OF SEQUENCES:
                                                           STREET: 6300 g
CITY: Chicago
STATE: Illino
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                               COUNTRY: United States of America ZIP: 60606-6402
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TELEPHONE: 312/474-0448
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OPERATING SYSTEM:
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                                                        Illinois
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Uehara, Hirotsugu
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                                                                                      Gerstein, Murray & Borun
South Wacker Drive
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APPLICATION NUMBER: US 08/362,577 FILING DATE: 27-MAR-1995 Clinical Isolate P2-2 E: Marshall, O'Toole, 6300 Sears Tower, 233 United States of America PatentIn Release #1.0, Version #1.25 Matsuhisa, Akio E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS Probe for Diagnosing Infectious Disease US/08/921,177 Score 14.4; Pred. No. 1 19036/32420 Mismatches Gerstein, Murray & Borun South Wacker Drive .1e+02; DB Length 9515; Indels 0; Gaps

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; STRAIN: Clinical Isolate P2-2
US-08-362-577C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                     FILING LALL.
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 29-AUG-199
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Probe for Diagnosing Infectious Disease NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
               NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
                                                                                                                                                                                                                                                                                     COUNTRY: United ZIP: 60606-6402
                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Rin-Laures, Li-Hsien REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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515 GCGCCGTTGCCAATCG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13, Application US/08920828
). 5853998
                                                                                                                                                                                                                                                                                                                                     Chicago
                                                                                                                                                                                                                                                                                                                      Illinois
                                                                                                                                                                                                                                                                                                                                                 E: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9515 base pairs
                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohno, Tsuneya
Matsuhisa, Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohno,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uehara, Hirotsugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            UMHER: US/08/920,828
29-AUG-1997
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93.8%;
                                                                                                  US 08/362,577
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                   Gerstein, Murray & Borun
South Wacker Drive
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; MOLECULE TYPE: Genomic DNA; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas aeruginosa; STRAIN: Clinical Isolate P2-2 US-08-920-828-13
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US-09-103-840A-2/c
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TITLE OF INVENTION: DNA SEQUENCES FOR TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/10 CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                        Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Patent No. 6294328
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Best Local :
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                                                                                                                           APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRA.
TITLE OF INVENTION: TUBERCULOSIS
TILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
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APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 9515 base pair
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1572527 TGCCGCCGTTGCCAAT 1572542
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TOPOLOGY: li
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l Similarity 93.8%;
15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%;
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Pred. No. 6
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                            FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
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Search completed: June 20, 2003, 23:25:32 Job time : 12.1792 secs
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US-09-103-840A-1
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                 Query Match 80.0
Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8%;
Matches 15; Conservative
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LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                               1572688 TGCCGCCGTTGCCAAT 1572703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGGCGCCGTTGCCAAT 16
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841864 TGGCGCCGTTGCCGAT 841849
                                                                                                                       1 TGGCGCCGTTGCCAAT 16
                                                                                                                                                               80.0%; Score 14.4; I
93.8%; Pred. No. 67;
tive 0; Mismatches
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Pred. No. 67;
                                                                                                                                                                                                       DB 4; Length 4411529;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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Gapop 10.0 , Gapext 1.0
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18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_NA: *
: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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    /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 19	c 17	c 16	c 15	c 14	c 13	c 12	c 11	c 10	ი 9	ი 8	c 7	6	5	4	ი ა	2	1	Result No.
14.8	14.8	14.8		14.8						14.8	14.8	14.8	14.8	14.8	15	18	18	Score
82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	82.2	83.3	100.0	100.0	Query Match
8095																		Length
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US-09-989-920-73	US-10-216-981A-2	US-10-003-152-13	US-10-002-304-13	US-10-002-050-13	US-10-003-152-21	US-10-002-304-21	US-10-002-050-21	US-10-003-152-11	US-10-002-304-11	US-10-002-050-11	US-09-974-300-764	US-09-938-842A-807	US-09-974-300-4705	US-09-878-574-15377	US-10-101-464A-479	US-09-965-553-36	US-09-965-553-1	ID
sequence 73, Appl	2, Ap	Sequence 13, Appl	-	7	Sequence 21, Appl	21,	Sequence 21, Appl	Sequence 11, Appl	11,	Sequence 11, Appl	Sequence 764, App	Sequence 807, App	Sequence 4705, Ap		Sequence 479, App	Sequence 36, Appl	Sequence 1, Appli	Description

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	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
	13.4	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	13.8	14	14	14.4	14.4	14.4
	74.4	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	76.7	77.8	77.8	80.0	80.0	80.0
	277	465237	13715	6378	6373	4588	3538	2940	1627	1405	1320	1078	897	897	897	576	538	538	476	365	174	3268	1392	1863	1854	943
	10	10	7	9	9	9	9	10	12	9	10	10	10	10	10	10	10	9	10	10	9	9	10	10	9	10
	US-09-294-093B-2256	US-09-933-267A-1	US-08-781-986A-195	US-10-037-270-332	US-10-000-512-1	US-10-114-170-26	US-09-952-267-10	US-09-801-368-283	US-10-062-254-237	US-10-122-822-6	US-09-815-242-9819	US-09-974-300-2700	US-09-841-132-132	US-09-841-132-130	US-09-841-132-120	US-09-974-300-5436	US-09-925-299-369	US-09-925-299-369	US-09-974-300-5603	US-09-880-107-357	US-10-122-822-21	US-09-927-827-24	US-09-815-242-9820	US-09-815-242-9985	US-09-894-844-103	US-09-822-830A-533
	Sequence 2256, Ap	Sequence 1, Appli	Sequence 195, App	Sequence 332, App	Sequence 1, Appli	Sequence 26, Appl	Sequence 10, Appl	Sequence 283, App	Sequence 237, App	Sequence 6, Appli	Sequence 9819, Ap	Sequence 2700, Ap			Sequence 120, App	Sequence 5436, Ap	Sequence 369, App	Sequence 369, App	Sequence 5603, Ap	Sequence 357, App	Sequence 21, Appl	Sequence 24, Appl	Sequence 9820, Ap	Sequence 9985, Ap	Sequence 103, App	Sequence 533, App

ALIGNMENTS

Query Match 100.0%; Score 18; DB 10; Length 18; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 TGGCGCCGTTGCCAATTG 18	US-09-965-553-1 ; Sequence 1, Application US/09965553 ; Patent No. US2002011259A1 ; GENERAL INFORMATION: ; APPLICANT: Wright, David A. ; APPLICANT: Voytas, Daniel F. ; TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto : FILE REPERFENCE. D-1065 THIED blant Potroelement
Db 1 TGGCGCCGTTGCCAATTG 18	CURRENT APPLICATION NUMBER: US/99/965,553 CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: 09/322,478 PRIOR FILING DATE: 1999-05-28 PRIOR PILING DATE: 1998-05-29 PRIOR APPLICATION NUMBER: 60/087125 PRIOR PILING DATE: 1998-05-29 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 18 TYPE: DNA ORGANISM: Glycine max -09-965-553-1 Query Match Best Local Similarity 100.0%; Score 18; DB 10; Length 18; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps TGGCGCCGTTGCCAATTG 18 TGCGCCCGTTGCCAATTG 18 TGCGCCCGTTGCCAATTG 18

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US-09-878-574-15377; Sequence 15377, Applicatio; Patent No. US20020110548A1
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SEQ ID NO 479
LENGTH: 412
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SEQ ID NO 36
LENGTH: 150
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: 09/322,478 PRIOR FILING DATE: 1999-05-28
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                 APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE REFERENCE: 38-21(15401)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                           GCGCCGTTGCCAATT 18
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                                                                                                                                                                                                                                                                                                                                                                                                           83.3%; Score 15; DB 9; 100.0%; Pred. No. 1e+02
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RESULT 6
US-09-938-842A-807
US-09-938-842A-807
; Sequence 807, Application US/09938842A
; Patent No. US20020160378A1
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; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701070032H2
US-09-878-574-15377
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US-09-974-300-4705
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US-09-974-300-4705
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APPLICANT: Berka, R
APPLICANT: Clausen
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PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 15377
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4705
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Best Local Similarity
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                                                     APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                   APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
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                                      PRIOR APPLICATION NUMBER: US 60/300,111
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FILING DATE: 2001-06-22 R OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 TGACGCCGTTGCCGATTG 304
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88.9%;
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Pred. No. 1.
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Pred. No. 1.
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; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-764
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-807
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                 SEQ ID NO 11
LENGTH: 2155
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/10002050 Publication No. US20030032095A1
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Best Local (
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                                                                                                                                             APPLICANT: Boldog, Ferenc
APPLICANT: Herrmann, John
TITLE OF INVENTION: NO. US20030032095A1el Nucleic Acid Sequences Encoding Human Sema;
FILE REFERENCE: 19966-554 Cura-54 CON-S14
FILE REFERENCE: 19966-554 Cura-54 CON-S14
CURRENT APPLICATION NUMBER: US/10/002,050
CURRENT FILING DATE: 2001-11-02
PRIOR FILING DATE: 2000-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                          PRIOR APPLICATION NUMBER: 60/140,584 PRIOR FILING DATE: 1999-06-23
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                                                                         SOFTWARE:
                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shimkets, Richard APPLICANT: Fernandes, Elma
ORGANISM: Homo sapiens
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Local Similarity 88.9%;
nes 16; Conservative
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Similarity 88.9%;
                                                                       PatentIn Ver.
                                                                                                                                                                                                                                                                                               Fernandes, Elma
Vernet, Corine
Yang, Meijia
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Pred. No. 1
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Pred. No. 1.4e+02;
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                                        APPLICANT: Fernandes, Elma
APPLICANT: Vernet, Corine
APPLICANT: Vang, Meijia
APPLICANT: Boldog, Ferenc
APPLICANT: Herrmann, John
TITLE OF INVENTION: No. US20020151494A1el Am
FILE REFERENCE: 15966-554 Cura-54 CON-512
CURRENT APPLICATION NUMBER: US/10/003,152
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
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US-10-002-304-11/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Best Local :
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TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
FILE REFERENCE: 15966-554 Cura-54 CON-S8
CURRENT APPLICATION NUMBER: US/10/002,304
CURRENT FILING DATE: 2001-11-02
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         PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: (166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 21
TYPE: DNA
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NAME/KEY: CDS
LOCATION: (166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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Vernet, Corine
Yang, Meijia
Boldog, Ferenc
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88.9%;
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Pred. No. 1.6e+02;
0; Mismatches 2;
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Pred. No. 1
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; NAME/KEY: CDS
; LOCATION: (166)..(1935)
US-10-003-152-11
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US-10-002-304-21/c
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LENGTH: 2156
                                                                                                               GENERAL INFORMATION:
                                                                                                                                   Sequence 21, Application US/10002304 Publication No. US20030036185A1
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Best Local Similarity
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                                                             APPLICANT: Shimkets, Richard APPLICANT: Fernandes, Elma APPLICANT: Vernet, Corine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Herrmann, John
TITLE OF INVENTION: NO. US20030032095Alel Nucleic Acid Sequences Encoding Human
FILE REFERENCE: 15966-554 CULTA-54 CON-S14
CURRENT APPLICATION NUMBER: US/10/002,050
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 09/604/286
PRIOR FILING DATE: 2000-06-22
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SOFTWARE: PatentIn Ver. 2.0
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PRIOR FILING DATE: 1999-06-23
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (166)..(2037)
NAME/KEY: variation
LOCATION: (1)..(2156)
OTHER INFORMATION: N may be any nucleotide
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INVENTION: Polynucleotides and polypeptides encoded thereby
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Similarity 88.9%;
                           Fernandes, Elma
Vernet, Corine
Yang, Meijia
Boldog, Ferenc
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Boldog, Ferenc
                 Herrmann,
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Pred. No. 1
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FEATURE:
NAME/KEY: CDS
LOCATION: (166)..(2037)
NAME/KEY: variation
LOCATION: (1)..(2156)
OTHER INFORMATION: N may be any nucleotide
US-10-003-152-21
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US-10-003-152-21/c
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SEQ ID NO 21
LENGTH: 2156
TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 2156
                                                                Matches
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/604,286
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boldog, Ferenc
APPLICANT: Herrmann, John
TITLE OF INVENTION: No. US20020151494A1e1
FILE REFERENCE: 15966-554 Cura-54 CON-S12
CURRENT APPLICATION NUMBER: US/10/003,152
CURRENT FILING DATE: 2001-11-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (166)..(2037)
NAME/KEY: variation
LOCATION: (1)..(2156)
OTHER INFORMATION: N may be any nucleotide
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                               1 TGGCGCCGTTGCCAATTG
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TGGCGCCGATGCCAGTTG 1281
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Vernet, Corine
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                                                                  Conservative
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88.9%;
                                                                Score 14.8; D
Pred. No. 1.6e
0; Mismatches
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Pred. No. 1.
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1.6e+02;
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                                                                                                  DB 12;
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RESULT 14

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RESULT 15
US-10-002-304-13/c
US-10-002-304-13/c
; Sequence 13, Application US/10002304
; Publication No. US20030036185A1
; GENERAL IMPORMATION:
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; OTHER INFORMATION: N may be US-10-002-304-13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                             APPLICANT: Hermann, John
TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
FILE REFERENCE: 15966-554 CURA-54 CON-58
CURRENT APPLICATION NUMBER: US/10/002,304
CURRENT FILING DATE: 2001-11-02
CURRENT FILING DATE: 2001-11-02
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TITLE OF INVENTION: NO. US20030032095A1el Nucleic Acid Sequences Encoding Human Semap
FILE REFERENCE: 15966-554 Cura-54 CON-S14
CURRENT APPLICATION NUMBER: US/10/002,050
CURRENT FILING DATE: 2001-11-02
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                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/140,584
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 49
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TYPE: DNA
ORGANISM: Homo sapiens
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                                  NAME/KEY: variation LOCATION: (1)..(2284)
                                                                       NAME/KEY: CDS
LOCATION: (166)..(1953)
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Yang, Meijia
Boldog, Ferenc
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Copyright (c) 1993 - 2003 Compugen Ltd
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SUMMARIES

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	RESULT 1 AF186184 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE		44444 0422 0422		32 32 32 32 32	16 17 18 19 20 21 22 23	1111 1111 1111 1111 1111 1111 1111 1111 1111	ult No.
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Embryophyta; Tracheophyta; dons; core eudicots; Papilionoideae; Phaseoleae;	linear PLN 10-SEP-2001 3-1, partial sequence.		ABL101304 ALBITOPS AB046431 Arabidops AF296831 Arabidops AF378079 Arabidops AL138663 Arabidops AB046436 Arabidops AC063973 Genomic S	Arak Arak Arak Sequ Sequ Arak	Pisu Pisu Nicc Arak Genc Arak Arak	Glycine Glycine Glycine Fisum sa Vicia fa Medicago Lotus ja	AF186184 Glycine m AF186182 Glycine m AF378068 Glycine m AF378063 Glycine m AF186183 Glycine m AF186183 Glycine m AF378063 Glycine m AF378064 Glycine m AF378072 Glycine m AF378070 Glycine m AF378070 Glycine m AF378073 Glycine m	scription

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Wright, D.A. and Voytas, D.F.
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AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
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/db_xref="taxon:3847"
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10128 bp DNA linear PLN Glycine max retrovirus-like element Calypsol-1, partial AF186182
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Submitted (14-SEP-1999) Zoology and Genetics, Ic
University, 2208 Molecular Biology Bldg., Ames,
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294. >10128
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/gene="pol"
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8068. .8976
/gene="envelope-like"
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Submitted (08-MAY-2001) Department of Zoology and Genetics,
State University, 2208 Molecular Biology, Ames, IA 50011, U
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Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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/variety="Williams"
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/db_xref="taxon:3847"
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Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
                                                                                                                                                                                                                                                                          Voytas,D.F. and Wright,D.A.

Direct Submission
Submitted (08-MAY-2001) Department of Zoology and Genetics, Id State University, 2208 Molecular Biology, Ames, IA 50011, USA
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/variety="L85"
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/db_xref="taxon:3847"
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Wright, D.A. and Voytas, D.F.
Direct Submission
Submitted (14-SEP-1999) Zoology and
University, 2208 Molecular Biology
                                                                                                                                                         Unpublished
2 (bases 1
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Glycine max retrovirus-like element
AF186183
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/strain="L85"
/db_xref="taxon:3847"
2321 2326
                /rpt_type=dispersed 2331. .4014 4017. .6900
                                         /note="polypurine tract"
2331    .12569
/rpt_family="retrovirus-like"//rpt_family="retrovirus"/retrovirus
         /gene="pol"
                                                                                                             ocation/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phas
1 (bases 1 to 763)
Wright, D.A. and Voytas, D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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2 (voytas,D.F. and Wright,D.A.
Direct Submission
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Direct Submission
Submitted (08-MAY-2001) Department of Zoology and Genetics,
State University, 2208 Molecular Biology, Ames, IA 50011, US
Location/Qualifiers
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/db_xref="taxon:3847"
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Wright, D.A. and Voytas, D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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Direct Submission
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/product="AAL06417.1"
/protein_id="AAL06417.1"
/db_xref="GI:15724028"
/translation="VRKEVLKLLEVGLIYPISDSAWVSPVLVVSKKEGMTVIRNEKND
LIPTRTVTSWKLCIDYRKLNEATRKDHFPLPFMDQMLERLAGHAYYCFLDAYFGYNQI
VVDPKDQEKNAFTCPFGVFAYERIPFGLCNAPTFTQMCMLAIFADIYEKSIEVFMDDF
SVFVPSLESCIKKLEMVLQRCVETNLYLNWEKCHFMVREGIVLGHKISTRGIEVDQTK
IDVIEKLPPPSNVKGIRSFLGQARFYRRFIKDFTKV"

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/db_xref="taxon:3847"
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/variety="L85"
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Pred. No. 1.5e-126;
0; Mismatches 105;
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449; Conser
                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (26-MAR-2002) Yasukazu Nakamura, Kazusa DNA Re Submittute, Department of Plant Gene Research; 1532-3, Ya Kisarazu, Chiba 292-0812, Japan (B-mail:yn@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T., Structural Analysis of a Lotus japonicus Genc Features and Mapping of Sixty-six TAC clones Regions of the Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lotus japonicus DNA, clone_lib:LjT library clone:LjT16I07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lotus japonicus genomic complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                               TTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACAC
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29650
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                         /organism="Lotus japonicus"
/db_xref="taxon:34305"
/chromosome="5"
/clone="LjT16107"
/clone=_lib="LjT library"
/note="TAC Clone:TM0040"
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Pred. No. 1.3e-103;
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Glycine max
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Elycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Voytas,D.F. and Wright,D.A.
Direct Submission
Submitted (08-MAY-2001) Department of Zoology at
State University, 2208 Molecular Biology, Ames,
Location/Qualifiers
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wright,D.A. and Voytas,D.F.
Athila4 of Arabidopsis and Calypso
endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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a 132 c
                                                                                                                                                                              /note="endogenous_virus: <1. .>762
                                                                                                                                                                                                           /isolate="Soybean5-1"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                       /organism="Glycine max"
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74.3%;
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endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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Voytas, D.F. and Wright, D.A.
Direct Submission
                                                                      ATTGGGAGAAATGTCATTTCATGGTCCAAGAAGGAATTATGTTGGGGCATAAAATTT 621
                                                                                   ATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCT
                                                                                                                  GTTGTTTGACCAATTTAGAGCTAGTGTTGAAGTACTGTGAGGAGACAAATTTAGTATTGA
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/db_xref="taxon:3847"
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voytas,D.F. and Wright,D.A.
Direct Submission
Submitted (08-MAY-2001) Department of Zoo.
State University, 2208 Molecular Biology,
Location/Qualifiers
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3 (bases 1 to 110729)
$\text{Shaull, S., Lin, S., Dixon, R.,} \text{Cook, D., Kim, D. and Roe, B.A.} \text{Direct Submission}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 110729)
1 (bases 1 to 110729)
Shaull,S., Lin,S., Dixon,R., May,G., Su
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-5n3
                                                                                                                                                                                                                                                                                                                                                                     Center: Department Of Chemistry
The University Of Oklahoma
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Submitted (31-MAY-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Cook, D., Kim, D. and Roe, B.
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Aug 3, 2002 this sequence version replaced gi:22002169
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63722 TTGAAGCCGGTATGATCTATCCAATCTCGGATAGCAAATGGGTAAGTCCGGTGCAAGTAG
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                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae
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(bases 1 to 13637)
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/db_xref="taxon:3880"
/clone="mth2-5n3"
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9 92571: contig of 11584 bp in
2 92671: gap of unknown length
10729: contig of 18058 bp in
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Wright, D.A. and Voytas, D.F.
Direct Submission
Submitted (14-SEP-1999) Zoology and Genetics, Id
University, 2208 Molecular Biology Bldg., Ames,
1. 13637
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            AATTGGGAGAAATTCCATTTCATGGTTCAAGAAGGAATAGTGCTGGGGGCATAAAATTTCA
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/note-"polypurine tract"
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/rpt_type=dispersed
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/strain="L85"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Embryophyta;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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AF378071
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Voytas,D.F. and Wright,D.A.
Direct Submission
Submitted (08-MAY-2001) Department of Zoology and Genetics,
State University, 2208 Molecular Biology, Ames, IA 50011, Using the Control of Coology and Genetics,
State University, 2208 Molecular Biology, Ames, IA 50011, Using the Coology and Genetics.
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Wright, D.A. and Voytas, D.F.
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endogenous plant retroviruses
Genome Res. 12 (1), 122-131 (2002)
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TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGACA
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Search Job tim	Db	Qy	Db	Qy	DЪ
Search completed: June 20, 2003, 23:24:00 Job time : 2522.09 secs	565 ATTGGGAGAAATGCCATTTCATGGTTCAAGAAGGAATAGTGCTGGGCCATAAAATTTCA 623	542 ATTGGGAAAAGTGTCATTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA 600	505 GCTACTTATCAAACCTTGAAAGAGTATTACAGAGATGTGAAGAGTCTAATCTAGTTCTCA 564	482 GCTGTTTGAGGAACCTAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGA 541	445 TGGAAAAATGCATTGAACTTTTCATGGACGATTTCTCTATTTTTGGGCCATCTTTTGAAG 504

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Title:
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                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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plants, especially soybean -
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RESULT 2
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                                                                                      retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least I agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that are used to transfer the nucleic acids
                                                                                                                                                                                                                                               The present sequence comprises a generic plant retroelement obtained from retrovirus like elements (retroelements) calypso of soybean, cyclops of pea and athila of Arabidopsis thaliana. The invention provides molecular tools in the form of retroelements and
                                                      Sequence 12286 BP;
                                                                                                                                                                                                                                                                                                                 Claim 1(h); Page 84-88; 118pp; English.
                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules for imparting characters to plants, especially soybean
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CDS
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Arabidopsis thaliana
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28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retrovirus; transgenic plant; gene transfer;
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99US-0087125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 1482..6887
                                                     3748 A; 2540 C;
100.0%; Score 600; DB 21; 100.0%; Pred. No. 3.5e-192; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               athila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyclops; ss
                                                      2767
                                                     G;
                                                                                                                                                                                                                                                                                                                                                 agronomically significant
                                                      3231
                                                     Τ,
                           Length 12286;
  Indels
                                                     0
                                                     other
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 Gaps
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This is the nucleotide sequence of the Calypso 1-3 retroelement soybean. It was identified by screening of a soybean lambda
                                                                                                                                                                                                                                   Retroelement;
Calypso 1-3;
                                                                                                                                                                                                                                                                                                                    AAZ35273 standard;
                                                                                                                                                                                                                    Glycine max
                                                                                                                                                                                                                                                               Soybean retroelement Calypso 1-3
                                                                        WPI; 2000-105586/09
                                                                                        Wright DA, Voytas DF
                                                                                                                                    29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                 W09960842-A2
                                                                                                                                                                                                                                                                                 27-MAR-2000
                          Example 3; Page 102-104; 118pp; English.
                                                                                                          (WRIG/) WRIGHT (VOYT/) VOYTAS
                                                                                                                                                               28-may-1999;
                                                      nucleic
                                                                                                                                                                                                                                                                                                                                                                                                   4758
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 4397
                                                                                                                                                                                                                                                                                                                                                                                AATTGGGAAAAGTGTCATTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCCATTTTTTCAGACATG
                                             6
                                            acid molecules for imparting to plants, especially soybean
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                   retrovirus; transgenic
soybean; ss.
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                                                                                                                                    98US-0087125
99US-0087125
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                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                    4609
                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                            plant;
                                                   agronomically significant
                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                             transfer;
          of.
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RESULT 4
AAZ35280
ID AAZ3
XX
AC AAZ3
XX
AC AAZ3

AAZ35280 standard;

DNA; 597

ВP

AAZ35280; 27-MAR-2000

(first entry)

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cretroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that particles are used to transfer the nucleic acids into plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4609 BP; 1420 A; 949 C; 1146 G; 1094 T; 0
                                                           1654
                                                                                                                           1594
                                                                                                                                                                                      1534
                                                                                                                                                                                                                                                     1474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1174 TTGGAGGTTGGGCTCATATACCCCCATCTGGACAACGCTTGGGTAAGCCCCAGTACAGGTG
                           541
                                                                                            481
                                                                                                                                                         421
                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                GTTCCCAAGAAAGGTGGAATGACAGTGGTACAAAATGAGAGGAATGACTTGATACCAACA
                                                                                                                                          GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGAC
                                                                                                                                                                                                     GGGTTATGTAATGCACCAGCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCACAAGATCTCA
                                                                             AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACACACTTGGTACTG
                                                                                                                           GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGAC
                                                                                                                                                                                      GGGTTATGTAATGTACCAGCCACATTTCAGAGGTGCATGCTGACCATTTTTTCAGACATG
                                                                                                                                                                                                                                                                                                                                                                               AGCTGTTTGAGGAACCTAGAAATGGTACTTCAGAGGTGCGTAGAGACTAACTTGGTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 571.2; DB 21;
Pred. No. 1.2e-182;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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1773
                                                                                            540
                                                                                                                           1653
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                                                            1713
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                                                                                                                                                                                                                                                                                    360
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Soybean retroelement calypso reverse transcriptase gene

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The present sequence represents the reverse transcriptase gene of cretrovirus-like element (retroelement) calypso of soybean. The cinvention provides molecular tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse H sequence (see AAZ35254-61). Also provided are plant retroviral particles that comprise a retrovirus protein encoded by a nucleic acid sequence encoding a plant retroviral envelope protein and a nucleic acid including e.g. the present sequence. These plant retroviral particles that compared to transfer the nucleic acid into plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 579; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 115; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules for imparting agronomically significant characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wright DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WRIG/) WRIGHT (VOYT/) VOYTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retroelement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 597
                                                                                         181
                                                                                                                                     181
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                                                                                                                                                                                                       GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
GTTCCCAAGAAAGGTGGAATGACAGTGGTACAAAATGAGAGGAATGACTTGATACCAACA
                                                                                                                                                                                                                                                                                                                                                                  TTGGAGGTTGGGCTCATATACCCCCATCTCTGACAACGCTTGGGTAAGCCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                       TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Voytas DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retrovirus;
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99US-0087125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.7%;
97.0%;
tive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 121 C; 158 G; 156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic
e; calypso;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 568.2;
Pred. No. 4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant; gene transfer;
soybean; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                      4e-182;
-~hes 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                 300
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RESULT 5
AAZ35271
ID AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX Soyl
DT 27-p
XX Soyl
XX Cal
XX Cal
XX Cal
XX W0:
XX Y W0:
XX Y W0:
XX Y Cal
XX X Cal
XX C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
This is the nucleotide sequence of the Calypso 1-1 retroelement of soybean. It was identified by screening of a soybean lambda ilbrary using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site retroelements include gag, pol, env and primer binding site invention provides molecular tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ35271 standard; DNA; 9829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules for imparting agronomically characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retroelement; retrovirus;
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(VOYT/) VOYTAS D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Voytas DF;
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                          02-DEC-1999
                                                  W09960842-A2
                                                                          Glycine max.
                                                                                                                                                                27-MAR-2000
                                                                                                                                                                                                                 AAZ35272
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  28-MAY-1999;
                                                                                                              Retroelement;
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                                                                                                                                       retroelement Calypso
                                                                                                                                                                                                                 standard;
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                                                                                                 soybean;
                                                                                                 retrovirus; transgenic soybean; ss.
 99WO-US11858
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                                                                                                                                                                                                                 DNA;
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Pred. No. 3.7e-169;
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                                                                                                              plant;
                                                                                                              gene transfer;
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Query Match Best Local Matches

559;

Conservative

Similarity

87.2%; 93.2%;

Score 523.2; DB Z1; Pred. No. 4.1e-166; Pred. No. 4.3e-166;

Indels

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Gaps

Length

12571;

1 TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG

TTGGAGGCTGGGCTCATATACCCCCTTCTCTAACAGTGCTTGGGTAAGCCCAGTACAGGTG

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4355

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GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGAC

GGGTTATGTAATGCACCAGCCACATTTCAGAGGTTCATGCTGGCCATTTTTTCAGACATG GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC TACTACTATTTCTTGGATGGATACTCGGGATATAATCAGATCGCGGTGGACCCCAGAGAT

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TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT

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360

В

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retroelement containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see AR35524-61). Also provided are plant retroviral particles that
                                                                                                                                                                                                                                                                          soybean. It was identified by screening of a soybean lambda library using a reverse transcriptuse probe. 2 Groups of soybea retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements invention provides molecular tools in the form of retroelements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecules for imparting characters to plants, especially soybean
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28-MAY-1999;
Sequence 12571 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WRIG/) WRIGHT (VOYT/) VOYTAS
                                   particles are used
                                                                                                                                                                                                                                                                                                                                                                                                                           is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Page 98-102; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence of the
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99US-0087125.
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3801 A; 2382 C; 2707 G; 3681 T;
                                       to transfer the nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agronomically significant
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0 other;
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Best Local Similarity
Matches 441; Conserv
                                                                                                         which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see ARZ35254-61). Also provided are plant retroviral particles that
                                                                                                                                                                                                                      retroelement containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line than the retroelement carries at least 1 agronomically-significant
                                                                                                                                                                                                                                                                                   soybean. It was identified by screening of a soybean lambda library using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements are invention provides molecular tools in the form of retroelements are
                                                                Sequence 9139 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-1998;
28-MAY-1999;
                                                                                             particles
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules for imparting agronomically significant characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroelement; retrovirus; transgenic plant; gene transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soybean retroelement Calypso
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                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 104-107; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wright DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WRIG/) WRIGHT D
(VOYT/) VOYTAS D
                                                                                                                                                                                                                                                                                                                                                                                                   is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2-1;
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                                                                                             are used to transfer the nucleic acids into plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Voytas DF;
                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide sequence of the Calypso 2-1 retroelement of
   Conservative
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99US-0087125
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                                                              2835 A; 1599 C; 2010 G;
              57.6%;
73.5%;
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Score 345.6;
Pred. No. 6.2e
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                WPI; 2000-105586/09
                                              Wright DA, Voytas DF
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28-MAY-1999;
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                                                                                                                                                                                                                                                                       Pisum sativum
                                                                                                                                                                                                                                                                                                                  Retroelement; retrovirus; transgenic plant; gene transfer
                                                                                                                                                                                                                                                                                                                                                 Pea retroelement cyclops reverse transcriptase
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                                                                             (WRIG/) WRIGHT (VOYT/) VOYTAS
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line
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                             AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATC
                                                                             AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGAGACTAACTTGGTACTG
                                                                                                                 AATGAGAAAACAATGGAAGTCTTCATGGATGACTTCTCGGTATTTGGTGTATCCTTTAGT
                                                                                                                                                                  GGGTTGTGCAATGCACCGACGACTTTCCAACGATGTGTGCAAGCCATTTTTGCCGACCTT
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              AATTGGTAGAAGTGCCACTTCATGGTGACCGAGGGGATAGTGCTTGGCCATAAAGTC
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Pred. No. 8.4e-96;
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RESULT 9 AAF22302/c

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18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct comprising a plant centromere, useful producing stably inherited michrosomes which can serve as vector the construction of transgenic plant and animal cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 102; Page 804-819; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCH-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Centromere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF22302 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-587529/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                          TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
CAAGAAAAAACCACTTTCACTTGTCCTTATGGGACCTTTGCTTACAAGCGTATGCCTTTC
                                   CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
                                                                                                               TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCCAGAGAT
                                                                                                                                                         AAAGACCATTTCCCATTGCCCTTCATTGATCAGATACTAGAAAGATTAGCAAACCATCCT
                                                                                                                                                                            AGGACTATAACTGGACATAGGATGTGTATTGACTATAGGAAGTTAAATGCTGCCTCTAGA
                                                                                                                                                                                                                                                                                                                     GTTCCTAAAAAAGGAGGTATGACAGTTGTTAAAAATTCTAAAGATGAACTGATACCCACT
                                                                                                                                                                                                                                                                                                                                                        GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAATGACTTGATACCAACA 120
                                                                                                                                                                                                                                                                                                                                                                                                 TTAGATGTTGGGGTTATCTACCCTATCTCTGATAGCACTTGGGTATCTCCAGTTCATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytokines,
                                                                            TACTATTGCTTTTTGTATGGTTATAGCGGATTTTTTCAAATCCCTATTCACCCAAATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               michrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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99US-0153584.
99US-0154603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeats from centromeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0125219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28943 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibodies, and growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerited michrosomes which can serve as vectors transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.3%;
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No. 1.5
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                                                                                            Best
                                                                                                        Query Match
                                                                                   Matches
                                                                                                                                                            The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting
                                                                                                                            Sequence 1082138 BP; 348775 A; 194404 C; 195515 G;
                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                  Claim 68;
                                                                                                                                                                                                                                                               Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                   Preuss
                                  1047007
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                                                                                                                                                                                                                                                                                                                                                                           (UYCH-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centromere;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana chromosome
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                                                                                             Local
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                                                                                417; Conserv
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TTAGATGTTGGGGTTATCTACCCTATCTCTGATAGCACTTGGGTATCTCCAGTTCATTGC 1047066
                                                                                                                                                     proteins such as hormones, enzymes, interleukins, cytokines, antibodies, and growth factors.
                                                TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                                                                                           Page 977-1388; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTGTTTGTTGAACCTGTGTAGGGTACTTAAAAGATGTGAAGAGACAAACATGGTGCTG 34593
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                                                                                                                                                                                                                                                                                                                                                  Copenhaver
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          michrosome; vector; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               99US-0125219.
99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
                                                                                           51.3%;
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                                                                                                                                                                                                                                                                                                                                                 Keith
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                                                                                         Score 307.8; DB 21; Pred. No. 5.9e-92;
                                                                              Mismatches
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                                                                              182;
                                                                            Indels
                                                                                                    Length
                                                                                                                          343444 T; 0 other;
                                                                                                    1082138;
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                                                                          Gaps
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   The present
                          Claim 36(a); Page 112-113; 118pp;
                                                                                                                                           (WRIG/)
(VOYT/)
                                                   New nucleic acid molecules for imparting characters to plants, especially soybean
                                                                                          WPI; 2000-105586/09
                                                                                                                 Wright DA, . Voytas DF;
                                                                                                                                                                                29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                     28-MAY-1999;
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                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                    Retroelement;
                                                                                                                                                                                                                                                                                                                                                          Arabidopsis
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                                                                                                                                         WRIGHT D A. VOYTAS D F.
                                                                                                                                                                                                                                                                                                                   transcriptase gene; athila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTC
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                                                                                                                                                                                                                                                                                                                                                        retroelement athila reverse transcriptase gene
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                retrovirus; transgenic plant;
                                                                                                                                                                              98US-0087125
99US-0087125
                                                                                                                                                                                                                   99WO-US11858
   represents
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                          English.
                                                           agronomically
transcriptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and intermetical contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tools in the form of retroelements and retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carries at least 1 agronomically-significant characteristic (ACS) In a preferred method, a helper cell line which expresses gag, po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retrovirus-like element (retroelement) athila of soybean. Athila was identified in a BLAST search of DNA sequences generated by the sequence of the sequence of the relation of the sequence of the sequence of Ty3/gypsy retrotransposons. The invention provides molecular
                                                                                                                                                                                       422
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                   ATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
                                                                       CATGTTTGTTGAATCTTGGCAGGGTATTGACTAGGTGCGAAGAGAGACGAATCTTGTTCTCA
                                                                                            GCTGTTTGAGGAACCTAGAGAGGGGTACTTCAGAGGTGCGAAGAGACACTAACTTGGTACTGA
                                                                                                                                                  TCGAGGAGATGGTGGAGGTTTTCATGGACGATTTTTCGGTCTATGGCCCCTCTTTCTCCT
                                                                                                                                                                                     TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACA
                                                                                                                                                                                                                                              GGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGG
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ATTGGGAAAAGTGTCATTTCATGGTGAAAGGAAGGCATAGTATTGGACCACAAGATATCA
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Pred. No. 1.
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AAF22281/c ID AAF22281 standard; I XX AC AAF22281;

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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a recombinant DNA construct of a pla (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 102; Page 351-364; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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              GGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTTCAGACATGG
                                                 AAGAAAAACCACTTTCACATGTCCCTACGGAACTTTTGCTTATAAGAGAATGTCATTTG
                                                                                                                                                                                                                                                                                                                                TGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTGG
GTTTATGTAATGCTCCTGCAACATTTCAGAGGTGTATGACCTCTATATTTTCAGATTTAA
                                                                                                                   ACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGATC
                                                                                                                                                                                 GAACTATAACTGGTCATAGAATGTGCATTGATTATAGGAAGTTAAAATGCTGCATCTAGGA
                                                                                                                                                                                                                                   TCCCTAAAAAGGGTGGAATGACTGTTGTCAAAAATGAAAAAGATGAACTAATCCCTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                      59590 BP; 17614 A; 12031 C; 13575
                                                                                                                                                          AAGATCATTTTCCTTTACCATTCATTGACCAAATGCTTGAACGTTTAGCTAATCATCCAT
                                                                                                                                                                                                                                                                                      TTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAATGACTTGATACCAACAC
                                                                                                      ACTATTGCTTTCTTGATGGATATAGTGGTTTCTTTCAAATACCAATTCACCCTAATGATC
                                                                            AGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCG
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                               The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                              Sequence 83390 BP;
                                                                                                                                                                                                                                                    Claim 102; Page 386-404; 1449pp; English.
                                                                                                                                                                                                                                                                           Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                    Preuss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC containing
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                                                                                                           Similarity
                                                        TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG
GTTCCTAAAAAGGGAGGTATGACAGTTGTTAAAAATGCTAAAGATGAACTGATACCCACT
                    GTTCCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAGGAATGACTTGATACCAACA
                                            TTAGATGCTGGGGTTATTTACCCTATCTCTGATAGCACTTGGGTATCTCCAGTTCACTGC
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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0; Mismatches
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                                                                                            Score 303; DB 21;
Pred. No. 6e-91;
0; Mismatches 185;
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                                                                                                                                                                          18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
The present invention relates to a (Arabidopsis thaliana) centromere.
                                                     Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors fithe construction of transgenic plant and animal cells
                                    Claim
                                                                                                                                Preuss
                                                                                                                                                                                                                                               17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                         Centromere; michrosome;
                                                                                                                                                      (UYCH-) UNIV CHICAGO.
                                                                                                                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                             WO200055325-A2
                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                              BAC containing repeats
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                                Page 529-549; 1449pp; English.
                                                                                                                               Copenhaver
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Best Local
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                                                                                                                    Centromere;
                                                                                                                                                                                                                  AAF22302 standard;
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the construction of transgenic plant and animal cells expressing
selected proteins such as hormones, enzymes, interleukins, clotting
factors, cytokines, antibodies, and growth factors.
18-MAR-1999;
                     17-MAR-2000; 2000WO-US07392
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                                                                                             Arabidopsis
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99US-0125219
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18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct comprising a plant centromere, producing stably inherited michrosomes which can serve at the construction of transgenic plant and animal cells
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CATGTTTGTTGAGTCTTGGCAGGTTATTGAGCAGGTGTGAGGAGACGAATCTTGTTCTCA
                                                                             GCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGGAGACTAACTTGGTACTGA 541
                                                                                                                                         TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGACA 481
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Pred. No. 6.5e-91;
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Search completed: June 20, 2003, 21:58:33
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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US-09-592-054-3
US-09-592-054-7
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•	•	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Ψ	Sequence 3, Appli	Sequence 53, Appl	Sequence 53, Appl	Sequence 2, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 3, Appli		Sequence 3, Appli	Sequence 33, Appl	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

Sequence 11, Application US/09322478

Patent No. 6331662

GENERAL INFORMATION:
APPLICANT: Wiight, David A.
APPLICANT: Wiight, David A.
APPLICANT: Woytes, Daniel F.
TITLE OF INVENTION: Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478

CURRENT APPLICATION NUMBER: US/09/322,478

CURRENT APPLICATION NUMBER: 60/087125

EARLIER APPLICATION NUMBER: 60/087125

EARLIER APPLICATION STATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 600

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
COURSE TO THE STATE OF SECTION OF A STATE OF A STATE OF SECTION OF A STATE OF ; OTHER INFORMATION: Description of Artificial ; OTHER INFORMATION: retroelement sequence US-09-322-478-11 Query Match
Best Local Similarity Matches 181 121 301 241 181 121 61 61 GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120 600; 1 TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG 1 TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA Conservative 100.0%; 0; Score 600; DB 4; Pred. No. 6.4e-199; Mismatches Sequence: 0 Length 600; Indels 0; Gaps 240 240 180 180 300 60

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Sequence 17, Application US/09322478

Patent No. 6331662

GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Wright, David A.
APPLICANT: Voytes, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478

CURRENT APPLICATION NUMBER: US/09/322,478

CURRENT FILING DATE: 1999-05-28

EARLIER APPLICATION NUMBER: 60/087125

EARLIER FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SOCTWARE: Patentin Ver. 2.0

SEQ ID NO 17

LENGTH: 12286

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                 GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
            GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
                                                         CAGGAGAAGACGGCCTTTACATGCCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
                                                                                                   TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT
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Conservative
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Pred. No. 3.8e-198;
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; ORGANISM: Glycine
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Matches
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SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
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AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTG
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US-09-322-478-34
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Best Local S
Matches 579
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LENGTH: 597
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Patent No. 6331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Plant Retroelements and Mether File Reference: p-1065 ISURF Plant Retroelement CURRENT APPLICATION NUMBER: US/09/322,478 CURRENT FILING DATE: 1999-05-28 EARLIER APPLICATION NUMBER: 60/087125 EARLIER APPLICATION NUMBER: 60/087125 EARLIER FILING DATE: 1998-05-29 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wright, David PAPPLICANT: Voytas, Daniel
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ORGANISM: Glycine
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                                                                                                                                               GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
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         AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATC 597
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Pred. No. 7.5e-188;
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GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Wright, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Rel
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
SEQ ID NO 19
LENGTH: 9829
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Matches 564;
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AATTTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCACAAGATCTCA 600
                                                                                                    GTGGAGAAGAGCATCGAGGTATTTATGGACGACTTCTGGATTTTTGGACCCTCATTTGAC
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Pred. No. 1.5e-174;
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US-09-322-478-20
; Sequence 20, Application
; Patent No. 6331662
; GENERAL INFORMATION:

US/09322478

APPLICANT: Wright,

David

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; ORGANISM: Glycine
US-09-322-478-20
                                                                                                                     Sequence 22, Application US/09322478 Patent No. 6331662 GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: P-1065 ISUBE Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
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SEQ ID NO 20
LENGTH: 12571
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Best Local Similarity
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Pred. No. 2.1e-171;
0; Mismatches 38;
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APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

FITE OF INVENTION: Plant Retroelements and Methods Rel

FILE REFERENCE: P-1065 ISURF PLANT Retroelement

CURRENT APPLICATION NUMBER: US/09/322,478

CURRENT FILING DATE: 1999-05-28

EARLIER APPLICATION NUMBER: 60/087125

EARLIER APPLICATION NUMBER: 50/087125

PARTIER FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 29

LENGTH: 597

TURE: NOW

Related

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GENERAL INFORMATION:

; ORGANISM: Pisum US-09-322-478-29

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TYPE: DNA

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Sequence 29, Appli
Patent No. 6331662
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Best Local
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SOFTWARE: Patentin
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Pred. No. 1.1e-109;
0; Mismatches 159;
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RESULT 9
US-09-322-478-27
; Sequence 27, Application
; Patent No. 6331662
; GENERAL INFORMATION:
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Best Local
Matches 42
                                                                                SEQ ID NO 27
LENGTH: 600
TYPE: DNA
ORGANISM: Arabidopsis thaliana
S-09-322-478-27
                                     Matches
                                                                                                                                                 APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
                                                                                                                                         SOFTWARE: PatentIn Ver.
                                     Local Similarity
nes 415; Conserv
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TGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTGG
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                                     Conservative
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                                              50.8%;
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70.4%;
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                               Score 304.6; Db *,
Pred. No. 4.1e-96;
""" amatches 184;
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Pred. No. 2.6e-99;
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                                                         Length
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; TYPE: DNA
; ORGANISM: Glycine
US-09-322-478-23
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                                                                                                                 Conservative
                                                                                                                          28.7%;
75.2%;
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TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACA 481
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                                                                                                   CATGTTTGTTGAATCTTGGCAGGGTATTGACTAGGTGCGAAGAGACGAATCTTGTTCTCA
                                                                                                                                                   GCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGA 541
                                                                                                                                                                                                  TCGAGGAGATGGTGGAGGTTTTCATGGACGATTTTTCGGTCTATGGCCCCCTCTTTCTCCT
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                                                                                                                                                                                                                                                                                                                                                     GGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGG
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APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods
FILE REFERENCE: P-1065 ISURE Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
                                                                  TGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACACGAACTGTCACTGGTTGGC
GAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCCTTAC
                                                                                                                                                            ACCCCATCTCTGACAGCGCTTGGGTAAGGCCCAGTACAGGTGGTTCCCAAGAAAGGTGGAA
                                                                                                                                      ACCCCATCTCAGATAGTGCGTGGGTTAGCCCGGTGCAGGTTGTTCTCAAGAAGGGAGGTA
                                                                                                                                                                                                                                                    Score 172.4; DB 4
Pred. No. 2.3e-49;
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US-08-855-449-2
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US-08-855-449-2/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 783
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 13-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD FOR IDENTIFYING THE SEX OF TITLE OF INVENTION: SPINACH BY DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                            Local Similarity
les 162; Conserv
                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCLLLELLING, ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
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                                        1051
                                                                                         1111 CAAATGTGCGTCGATTACAGATATCTTAACACGACTAGCCCTAAAGACGATTTTCCACTG 1052
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GGATACTCGGGATACAACCAGATCGCGGTAGACCCCCAGAGATCAGGAGAAGACGGCCTTT 318
                                                         GATACTCGGGATACAACCAGATCGCGGTAGACCCCCAGAGATCAGGA 305
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                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: JP 119124/1996
14-MAY-1996
                                                                                                                                                                                                                                                                                                double
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                                                                                                                                                                      Score 69; DB 2;
Pred. No. 6.6e-14;
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                                                                                                                                                         Mismatches 155;
                                                                                                                                                                                   Length 1347
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                                                                  Matches
                                                                                              Query Match
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7568 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,
FILING DATE: 09-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                    NAME: Woessner, Warren REGISTRATION NUMBER: 30
                                                              Local Similarity ss 213; Conserv
                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box : CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
5482 GACTGGTTTTCAATTACAAGAGGCTAAATGACAACACATGGCCGGATCAATATTCATTGC
                  140 GAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCTTAC
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P.O. Box 2938
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                                                                  Conservative
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Somers, D. A.
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                                                                                                                                                              linear
                                                                                                                                            Genomic DNA
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                                                                             9.28;
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                                                                                                                                                                                                                                                                                                                     600.369US1
                                                           Score 55.4; DB 2;
Pred. No. 9.8e-09;
); Mismatches 241
                                                                                          Length 7568;
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APPLICANT: Olszewski, N.
APPLICANT: Tzafrir, I.
APPLICANT: Somers, D.A.
APPLICANT: Somers, D.A.
APPLICANT: Lockhart, B.
APPLICANT: Lockhart, B.
APPLICANT: Torbert, K.
TITLE OF INVENTION: Sugarcane bacilliform virus profile Reference: 600.369US2
CURRENT APPLICATION NUMBER: US/09/349,546
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: US 08/694,869
EARLIER FILING DATE: 1996-08-09
EARLIER FILING DATE: 1997-08-13
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US-09-349-546-2
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                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 7568
                                                                                                                                                                                                                                                                            Query Match
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SOFTWARE: FastSEQ for Wir
                                                                                                                                                                                                                                               Local Similarity
les 213; Conserva
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                                                 5602 TGAAGAGCGGGTTTCATCAAGTCGCCATGGATGAAGAAAGTATTCCATTAACAGCATTTT
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 CATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGGTTATGTAATGCACCAG
                                                                                                                                  GACTGGTTTTCAATTACAAGAGGCTAAATGACAACACATGGCCGGATCAATATTCATTGC
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                                                                                GATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGATCAGGAGAAGACGGCCTTTA
                                                                                                                CCGGAATCAATGCTCTACTAAAAAATGTTGCAAGAGCAAAGATCTTCTCAAAGTTTGATT
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                                                                                                                                                                                                                                          Score 55.4; DB 3;
Pred. No. 9.8e-09;
0; Mismatches 241;
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RESULT 15
US-09-592-054-5
; Sequence 5, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
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US-09-360-186-1/c
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APPLICANT: Staskawicz, et al.
TITLE OF INVENTION: Bs2 Resistance Gene
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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ORGANISM: Capsicum
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GTATTTATTGATAATATTCTGATCTAT
                              GTATTTATGGACGACTTCTCGGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCCTTCATGGATCTTATGAGTAGAGTGTTCCGTCAATTTATTGACTTGTTCGTCATT 24008
                                                                                                                                                      GCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGGTGGAGAAAAGCATCGAG
                                                                                                                                                                                                          CGAACCCGATATGGTCACTACAAATTTTTAGTCATGTCCTTCGGGTTGAGTAACGCCCCT
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                                                                                                                                                                                                                                                                                                                   CTTCGTTCGGGTTACCATCAGTTGAAAATTAGGGAGTCAGACATACCCAAGACAGCCTTC
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Pred. No. 5.3e-06;
0; Mismatches 174;
23981
                                                 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
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APPLICANT: Beraud, Christophe
APPLICANT: Finer, Jeffrey
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6440684el motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERNCE: 1016
CURRENT APPLICATION NUMBER: US/09/592,054
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENCTH: 1421
TYPE: DNA
ORGANISM: Human
US-09-592-054-5
                                                                                                                  VQ.
Search completed: June 20, 2003, 23:25:48 Job time: 76.6415 secs
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                                                                                                                                                                                                                                                                                                                  Query Match 5.6
Best Local Similarity 51.7
Matches 77; Conservative
                                                                                                                                                                                                                                      484 TACGAGAGGATCCTAAGGAAGGCATAAAGATTGTGGGACTCACTGAGAAGACTGTTTTGG 543
                                                                              604 CGGCTATGAACTCCCAGTCGTCCCGATCT 632
                                                                                                                                                                                 173 CCACACGGAAGGACCATTTCCCCTTACCT 201
                                                                                                                                                        544 TIGCCTIGGATACIGITITCCIGITIGGAACAGGGCAACAACICTAGGACIGIGGCCICCA 603
                                                                                                                                                                                                                                                             53 TACAGGTGGTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGGAATGACTTGA 112
                                                                                                                                                                                                                                                                                                                                          5.6%;
                                                                                                                                                                                                                                                                                                                  ; Score 33.8; DB 4; Length 1421; Pred. No. 0.12; 0; Mismatches 72; Indels 0
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Title:
Perfect score:
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          571.2
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1: /cgn2_6/ptodata/2/pubpna/US07_PUI
2: /cgn2_6/ptodata/2/pubpna/US06_NEW
3: /cgn2_6/ptodata/2/pubpna/US06_NEW
4: /cgn2_6/ptodata/2/pubpna/US06_NEW
4: /cgn2_6/ptodata/2/pubpna/US07_NEW
6: /cgn2_6/ptodata/2/pubpna/US08_NEW
6: /cgn2_6/ptodata/2/pubpna/US08_NEW
6: /cgn2_6/ptodata/2/pubpna/US08_NEW
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9: /cgn2_6/ptodata/2/pubpna/US09_NEW
10: /cgn2_6/ptodata/2/pubpna/US09_NEW
11: /cgn2_6/ptodata/2/pubpna/US10_NEW
12: /cgn2_6/ptodata/2/pubpna/US10_NEW
13: /cgn2_6/ptodata/2/pubpna/US10_NEW
14: /cgn2_6/ptodata/2/pubpna/US09_NEW
15: /cgn2_6/ptodata/2/pubpna/US09_NEW
16: /cgn2_6/ptodata/2/pubpna/US09_NEW
17: /cgn2_6/ptodata/2/pubpna/US09_NEW
18: /cgn2_6/ptodata/2/pubpna/US09_NEW
19: /cgn2_6/ptodata/2/pubpna/US09_NEW
19: /cgn2_6/ptodata/2/pubpna/US00_NEW
19: /cgn2_6/ptodata/2/pubpna/US00_NEW
10: /cgn2_6/p
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600
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100.0
195.2
94.7
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52.3
552.3
552.3
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:/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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:/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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                                  DB
          0 US-09-965-553-11
0 US-09-965-553-27
0 US-09-965-553-34
0 US-09-965-553-19
0 US-09-965-553-29
0 US-09-965-553-29
0 US-09-965-553-29
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0 US-09-965-553-27
0 US-09-965-553-27
0 US-09-965-553-27
0 US-09-965-553-16
US-09-997-672-1
US-09-997-672-1
US-09-997-672-1
0 US-09-964-680-1
0 US-09-964-680-1
0 US-09-864-680-1
0 US-09-864-680-1
0 US-09-864-680-1
0 US-09-864-684-152
0 US-10-184-644-152
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3971.420 Million cell updates/sec
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Compugen Ltd
Sequence 11, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 182, App
Sequence 152, App
Sequence 152, App
Sequence 152, App
Sequence 152, App
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
30.6	30.6	30.6	30.6	30.8	30.8	31	31	31.4	31.4	31.4	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33.4
5.1							5.2																		5.6
6271	699	699	472	809	809	1629	1584	671	671	500	2187	470	425	408	379	378	377	360	360	360	360	360	360	360	1355
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US-09-993-292A-1	US-10-184-634-138	US-10-184-644-138	US-09-918-995-33903	US-10-205-428-181	US-09-764-891-2253	US-09-732-224-6	US-09-732-224-3	US-10-184-634-346	US-10-184-644-346	US-09-925-300-825	US-10-175-523-110	US-09-918-995-8924	US-09-960-352-2591	US-09-960-352-10425	US-09-960-352-9011	US-09-960-352-12818	US-09-960-352-9257	US-09-822-827-438	US-09-780-669-438	US-09-759-143-438	US-10-010-940-438	US-09-895-814-438	US-09-895-793-438	US-10-012-896-438	US-10-021-577-1
Sequence 1, Appli	Sequence 138, App	Sequence 138, App	Sequence 33903, A	Sequence 181, App	Sequence 2253, Ap	Sequence 6, Appli	Sequence 3, Appli	Sequence 346, App	Sequence 346, App	Sequence 825, App	Sequence 110, App	Sequence 8924, Ap	Sequence 2591, Ap	Sequence 10425, A	Sequence 9011, Ap	Sequence 12818, A	Sequence 9257, Ap	Sequence 438, App	Sequence 438, App	Sequence 438, App	Sequence 438, App	•	Sequence 438, App	Sequence 438, App	Sequence 1, Appli

OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: retroelement sequence US-09-965-553-11 RESULT 1 US-09-965-553-11 GENERAL INFORMATION: APPLICANT: Wright, David A. APPLICANT: Wright, David A. APPLICANT: Voytas, Daniel F. TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto FILE REFERENCE: P-1065 ISURF Plant Retroelement CURRENT ELING DATE: U01-09-27 PRIOR APPLICATION NUMBER: 09/322.478 PRIOR FILING DATE: 1999-05-28 PRIOR FILING DATE: 1999-05-28 PRIOR FILING DATE: 1999-05-28 PRIOR APPLICATION NUMBER: 60/087125 PRIOR FILING DATE: 1998-05-29 NUMBER OF SEQ ID NOS: 41 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 11 Sequence 11, Application US/09965553 Patent No. US20020112259A1 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: LENGTH: 600 plant

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Matches 600;

Conservative

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Query Match Best Local Similarity

100.0%; 0;

Score 600; DB 10; Pred. No. 4.9e-197; Mismatches

Indels

0;

Gaps

Qy

121 121 61 61

GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAAGAATGACTTGATACCAACA 120

120

60

TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG 60 TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG

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APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

ITILE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322.478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 12286
TYPE: DNA
TYPE: DNA
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US-09-965-553-17
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Best Local S
Matches 600
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Patent No. US20020112259A1
GENERAL INFORMATION:
Application
                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                      121
                  181
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                                                                                                                                                                                                                     Similarity
                                        GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGGAATGACTTGATACCAACA
                                                                                                                                                    TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG
                                                                                                                                                                              TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTGTTTGAGGAACCTAGAGAGGGGTACTTCAGAGGTGCGAAGAGAGACTAACTTGGTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTGGGAAAAGTGTCATTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
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                                                                                                                                                                                                      100.0%; Score 600; DB 10; 100.0%; Pred. No. 2.3e-196; tive 0; Mismatches 0;
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APPLICANT: Wright, David A.
APPLICANT: Woytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Rel
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087125
PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
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Best Local Similarity
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TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT
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97.0%;
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APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: Plant Retroelements and Methods Rel

FILE REFERENCE: P-1065 ISURF Plant Retroelement

CURRENT APPLICATION NUMBER: US/09/965,553

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/322,478

PRIOR FILING DATE: 1999-05-28

PRIOR FILING DATE: 1999-05-29

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SECTIMARE: Patentin Ver. 2.0
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US-09-965-553-34
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LENGTH: 597
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                                                                            TACTACTGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCAGAGAT 300
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Pred. No. 4.9e-186;
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US-09-965-553-19
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US-09-965-553-19
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GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCCTCATTTGAC
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APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: Plant Retroelements and Methods Rel

FILE REFERENCE: P-1065 ISURF Plant Retroelement

CURRENT APPLICATION NUMBER: U5/09/985,553

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/322,478

PRIOR APPLICATION NUMBER: 09/322,478

PRIOR FILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 06/087125

PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 19

LENGTH: 9829
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Patent No. US20020112259A1
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94.0%;
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Pred. No. 6.8e-173;
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PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 12571
TYPE: DNA
ORGANISM: Glycine max
US-09-965-553-20
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US-09-965-553-20
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Patent No. US20020112259A1
GENERRAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURE Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT EILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
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Pred. No. 8.5e-170;
0; Mismatches 38;
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; ORGANISM: Glycine
US-09-965-553-22
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SEQ ID NO 22
LENGTH: 9139
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APPLICANT: Woytas, Daniel F.
APPLICANI: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
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Similarity 73.5%;
                              AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCCATAGTCCTAGGCCCACAAGATCTCA
                                                                                                                                                GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGAC
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AATTIGGGAGAAATTICCATTITCATGGTTCAAGAAGGAATAGTGCTGGGGGCATAAAATTTCA
                                                                GGGTGCCTATITAAATCTTGAAAGAGTATTACAGAGATGTGAAGAGTCCAATCTAGTTCTC
                                                                                             AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTG
                                                                                                                               GTGGAAAAATGCATCGAAGTTTTCATGGATGATTTCTCTATTTTTGGGCCCATCCTTTAAG
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Pred. No. 2e-108;
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APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Rel
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Pisum
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AATTGGTAGAAGTGCCACTTCATGGTGACCGAGGGGATAGTGCTTGGCCATAAAGTC
                             AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATC
                                                          TTATGCTTGGCAAACTTGAAAACGGTGCTTGAAAGATGTGTGAAGACCAATCTTGTGCTT
                                                                                                                    AATGAGAAAACAATGGAAGTCTTCATGGATGACTTCTCGGTATTTGGTGTATCCTTTAGT 480
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RESULT 9 US-09-965-553-27 ; Sequence 27, Ap

Application

us/09965553

RESULT 10 US-09-965-553-23

Sequence 23, Application US/09965553
Patent No. US20020112259A1
GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Woytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto

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PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
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GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Metl
FILE REFERENCE: P-1065 ISURF Plant Retroelement
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Best Local
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CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILING DATE: 1999-05-28
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                        122 GAACTATAACTGGTCATAGAATGTGCATAGATTATAGGAAGTTGAACGCTGCATCTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415;
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                                                                                                                                                                                                        GGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGG
                                                          TTGATGCTGGTGTCATCTACCCTATCTCTGATAGTACTTGGGTTTCTCCAGTGCATTGCG
                                                                                                                                                                                                                                                                                                                                           ACTACTGTTTCTTGGATGGATACTCGGGGATACAACCAGATCGCGGTAGACCCCAGAGATC
ATTGGGAAAAGTGTCATTTCATGGTGAAGGAAGGCATAGTATTGGACCACAAGATATCA
                            ATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA 600
                                                                                                                          TCGAGGAGATGGTGGAGGTTTTCATGGACGATTTTTCGGTCTATGGCCCCTCTTTCTCCT
                                                                                                                                                          TGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGGTTTTTTGGACCCTCATTTGACA 481
                                                                                                                                                                                          GTTTATGCAATGCTCCTGCAACATTTCAGAGGTGTATGACCTCTATATTTTCAGACTTAA
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CURRENT FILLING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR FILLING DATE: 1999-05-28
PRIOR FILLING DATE: 1999-05-28
PRIOR FILLING DATE: 1998-05-29
NUMBER: 07 SEQ ID NOS: 41
NUMBER: 07 SEQ ID NOS: 41
NUMBER: 07 SEQ ID NOS: 41
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; ORGANISM: Glycine max
US-09-965-553-23
                                                                                                                                                                                                                                                                                                                Sequence 634, Application US/10083357
Publication No. US20030054370A1
GENERAL INFORMATION:
APPLICANT: QLANDONG Zeng et al.
TITLE OF INVENTION: Systemic Discovery of
FILE REFERENCE: 032796-090
CURRENT APPLICATION UNMER: US/10/083,357
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1346
SEQ ID NO 634
LENGTH: 3813
TYPE: DNA
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SEQ ID NO 23
LENGTH: 10482
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Best Local Similarity
Matches 215; Conserv
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 TTGCATAGTGGTTACCACCAGATCCCGATGGAACCCCAAAGACCGCTACAAAACCGCCTTT
                                                                                 CGACTCTGCGTCGATTACCGCACCCTGAACAAAGCTACCATCTCCGACCCATTCCCCATTA
                                                                                                                               CGAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACGGAAGGACCATTTCCCCTTA 198
                GGATACTCGGGATACAACCAGATCGCGGTAGACCCCCAGAGATCAGGAGAAGACGGCCTTT 318
                                                      CCCAGAATCGACAACCTATTGAGCCGTATTGGAAATGCCCCAGATATTTACCACGCTAGAT
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75.2%;
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                                                                                                                                                                                     Score 80.8; DB 9;
Pred. No. 5.3e-17;
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Pred. No. 1.8
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US-10-255-536-16
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Query Match 11.48;
Best Local Similarity 46.68;
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Publication No. US20030087807A1
GENERAL INFORMATION:
APPLICANT: Greenspan, Ralph J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/255,536
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/09/669,751
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR APPLICATION NUMBER: US 60/168,579
PRIOR FILING DATE: 1999-12-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 GACAAATTTCCACCTTCCAAGAATAGAAGATATTCTTGATCAATTAGGAAGAGCAAAGTAT
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                                      GAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGACAGC 483
CCATCGCAAGCATTTCTATATATGGATGACTTAGTAGTAATAGGTTGTTCAGAAAAACAT
                                                                                                                     CTGAAAGTAGCACCAAACTCCTTCCAACGTATGATGACACTTGCATTTTCTGGTCTTGAA
                                                                                                                                                                              TTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATGGTG 423
                                                                                                                                                                                                                                                                                                    GAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGG 363
                                                                                                                                                                                                                                                                                                                                                                   TTTTCATGTCTCGACCTAATGTCTGGATTCCACCAGATAGAACTAGAAAAAGGTATAGA 284
                                                                                                                                                                                                                                       GATATAACGTCATTTTCAACAGCCAATGGCTCATATCGCTTCACGCGATTACCATACGGA
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Pred. No. 4.1e-13;
0; Mismatches 251
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; NAME/KEY: promoter;
; LOCATION: (1).. (4298)
; OTHER INFORMATION: Scarlet Runner;
; NAME/KEY: modified_base;
; LOCATION: (1).. (4298)
; OTHER INFORMATION: n = g, a, c or US-09-997-672-1
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Best Local Similarity 46.3%;
Matches 211; Conservative
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CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,672
PRIOR FILING DATE: 2000-11-28
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APPLICANT: Apuya, Nestor
APPLICANT: Tatarinova, Ta
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636 TAGTAAAACCCTAGAAGACCATCTAAGTCACCTTAGGGAAGTTCTTCTAGTTCTTAGGAA
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                                      TGGACCCTCATTTGACAGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGA 524
                                                                                                     CATTTTTTCAGACATGGTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTT 464
                                                                                                                                                                                            CAGAAGGATGCCATTCGGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGC
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                                                                                                                                                                                                                                                                                                                 ATTGCATGGGTCAACTCTATTCTCCAAAATTGACCTTAAAAGTGGATATCACCAAATTCG
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Tatarinova, Tatiana
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The Regents of the University of California
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Pred. No.
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US-09-997-672-2
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SEQ ID NO 2
LENGTH: 4921
TYPE: DNA
ORGANISM: Phaseolus coccineus
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Publication No. US20030061632A1
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TITLE OF INVENTION: Polynucleotides Useful
FILE REFERENCE: 023070-115810US
CURRENT APPLICATION NUMBER: US/09/997,672
CURRENT FILLING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/253,672
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 42
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NAME/KEY: modified_base
LOCATION: (1)..(4921)
OTHER INFORMATION: n = g,
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LOCATION: (4347)..(4509)
NAME/KEY: exon
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                                  465 TGGACCCTCATTTGACAGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGA 524
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Similarity 46.3%;
11; Conservative
TAGTAAAACCCTAGAAGACCATCTAAGTCACCTTAGGGAAGTTCTTCTAGTTCTTAGGAA 695
                                                                                                               CATTTTTTCAGACATGGTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTT 464
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                                                                                                                                                                                          CAGAAGGATGCCATTCGGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGC
                                                                          AATCAAGGAGGGTGATGAGTGGAAAACCGCTTTTAAGACCAAATTTGGATTATATGAGTG
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Tatarinova, Tatiana
Goldberg, Robert B.
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Pred. No.
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Sequence 1, Application US/09864680

Patent No, US20020012981A1

GENERAL INFORMATION:
APPLICANT: Staskawicz, et al.

TITLE OF INVENTION: Bs2 Resistance Gene
FILE REFERENCE: 50687

CURRENT APPLICATION NUMBER: US/09/864,680

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: 09/360,186

PRIOR FILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 31491

TYPE: DNA

ORGANISM: Capsicum annuum

US-09-864-680-1
Search completed: June 21, 2003, 00:34:41 Job time: 222.698 secs
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US-09-864-680-1/c
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Best Local Similarity 46.8%;
Matches 153; Conservative
                                                                           24007 GTATTTATTGATAATATTCTGATCTAT 23981
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                                                                                                                 439 GTATTTATGGACGACTTCTCGGTTTTT 465
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Pred. No. 2.1e-05;
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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308.8	310.4	310.4	315.2	315.2	317	Query Score Match Length
51.5	51.7	51.7	52.5	52.5	52.8	Query Match Length DB ID
762	834	759	841	727	582	1
17	17	17	17	17	17	: BB
ВН497441	BH435343	BH655348	BH718174	BH423185	BH421575	DB ID
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вн523876	вн709535	вн589626	вн484943	вн694557	вн479539	вн734399	BH543949	вн588426	вн661378	вн405540	вн536770	вн508673	вн580975	ВН576412	ВН654786	AQ956471	вн576493	BH452427	вн505270	BH554612	вн701377	ВН449694	BH244881	вн550351	вн682723	BH530743	вн434092	вн656439	BH420759	. во	BH443545	0165	вн703456	11	вн597975	. вн697068	BH714463	вн448511
6 BOHTW89TR	5 BOMAG18TR		3 BOGLI32TR	7 BOHVI20TR									5 BOGDR46TF											1 BOHAK33TR					BOGIJ23T			восон29т			5 BOHGL95TR			1 BOGOM52TF

ALIGNMENTS

FEATURES source			COMMENT	TITLE TOTRNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 BH421575/c
Location/Qualifiers 1582	Email: Cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TF Class: sheared ends.	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208	Other_GSSs: BOHEX22TR Contact: Chris Town	Whole genome shotgun sequencing of Brassica oleracea	Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.	Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 582)	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Brassica oleracea	Brassica oleracea.	GSS.	BH421575.1 GI:17607303	sequence. BH421575	F BOHE Brassica oleracea genomic clone BOHE	EH421575 - 582 55 TNA 110001 GSG 12-DEC-2001

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RESULT 2
BH423185/c
LOCUS
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ORGANISM
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VERSION
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          COMMENT
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                               AUTHORS
TITLE
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Best Local Similarity
Matches 416; Conserv
sequence.

N. BH423185

BH423185

GSS.

Brassica oleracea.

Enassica oleracea

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; eore eudicots; Spermatophyta; Brassicales; Brassicaceae; Brassica.

Enassica oleracea

(bases 1 to 727)

S Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other_GSSs: BOHHA57TF
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/strain="To1000DH3"
/db_xref="taxon:3712"
/clone="BOHEX22"
/clone="BOHEX22"
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/clone="POHEX22"
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/c
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71.6%;
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Pred. No. 1e-87;
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sequence.
BH718174
BH718174.1
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                                  BH718174
BOMGI87TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                    AATTGGGAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA
                                                                                                                                                     GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCCTCATTTGAC
                                                                                                                                                                                                                                                           GGGTTATGTAATGCACCACCACATTTCAGAGGTGCATGCTGGCCATTTTTTCAGACATG
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                                                                                                        AACTGGGAAAAGTGTCACTTCATGGTCAAAGAAGGGATTGTGCTGGGGGCACAAGATTTCA
                                                                                                                                                                           AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTG
                                                                                                                                                                                                  ATTGAGGATGTTGTGGAGGTGTTCATGGATGTTTCTCCGTCTATGGATCTTCGTTTTCT
                                                                                                                                                                                                                                                GGTCTATGTAATGCTCCAGCCACCTTTCAAAGGTGCATGATGTCGATCTTTTCTGATCTG
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/strain="701000BH3"
/db_xref="taxon:3712"
/clone="BOHHA57"
/clone=lib="BOHH"
/note="Vector: pHOS1; Site_1: Bst1
genomic DNA inserted into pHOS1 us
a 166 c 127 g 209 t
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1. 727
                                  BO_2_3_KB
  GI:18816340
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70.3%;
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                                    Brassica
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Pred. No. 4.
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                                    bp DNZ
oleracea
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4.1e-87;
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using BstXI
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                                    clone
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                                   GSS 20-FI
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Traci
Spermatophyta; Magnoliophyta; eudicotyledons; core eudico:
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica

1 (bases 1 to 841)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: TF
Class: sheared ends
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Brassica oleracea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                     GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCTCATTTGAC
                                                                                                                                      GGGTTATGTAATGCACCAGCCACATTTTCAGAGGTGCATGCTGGCCCATTTTTTTCAGACATG
                                                                                                                                                                                        CAGGAGAAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTC
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                                     AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGGTGCGAAGAGACTAACTTGGTACTG
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                       GCTTGTTTGTCAAATTTGTGCAGGGTCCTAGAGAGATGTGAAGACACCAACCTTGTGCTG
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/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMGI87"
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
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Pred. No. 4.4
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1 (bases 1 to 759)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
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Tel: 301-838-3523
Fax: 301-838-0208
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BH655348
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DNA is from a doubled haploid
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                   GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTTCAGACATG
                                                                              CAAGAGAAGACAATTCACCTGCCCATACGGTACTTTTGCCTACAGGAGAATGCCTTTC
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GGATTGTGCAATGCTCCTGCCACTTTCCAGAGATGCATGATGTCGATCTATACTGATCTT
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/Clone_lib="BO_2_3_KB"
/clone_lib="BO_2_3_KB"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1 using BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
187 c 163 g 209 t
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/strain="TO1000DH3"
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Pred. No. 1.3e-85;
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Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TF
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                                                                                                                                                                                                                                                                                                                                                                                                                    Class: sheared ends.
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             AGAACAATCACAGGGCATAGGATGTGCATTGACTACAGGAAGCTAAACTCAGCCACAAGG
                                                                                                      GTTCCTAAGAAGGGTGGCATCACTGTCATCACAAATGAGAAGGATGAGCTGATTCCTACC
                                                                                                                       GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGAAGA 120
                                                                                                                                                          TTGAGTGCAGGGGTGATCTACCCAATTTCAGACAGTACTTGGGTGAGCCCGGTTCATGTG
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AAGGACCACTTCCCACTTCCTTTCATTGACCAGATGCTGGAAAGACTAGCCAACCACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medical Center Drive,
                                                                                                                                                                                                                                                                             /CLONE_11b="BOHA"
/clone_11b="BOHA"
/note="Vector: pHOS1; &
genomic DNA inserted ir
genomic DNA inserted ir
179 g
                                                                                                                                                                                                                                                                                                                                  /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHAU19"
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                                                                                                                                                                                                                Score 310.4; DB 17;
Pred. No. 1.4e-85;
0; Mismatches 181;
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one BOHAU19, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica oleracea
EUKaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 762)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOHBD637F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH497441
BOHBD63TR
                                                                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica oleracea
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                                                  TTGGAGGCTGGGCTCATATACCCCATCTCTGACAGCGCTTGGGTAAGCCCCAGTACAGGTG
GTTCCCAAGAAAGGTGGAATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACA 120
                             TTAGATGCAGGAGTAATATATCCTATTTCAGATAGCAAATGGGTGTCTCCTGTGCATGTT
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                                                                                                                                                                                                                                                                                                                                              primer: TR
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                                                                                                                                                                                                                                                                                                                               sheared ends.
                                                                                                                                                                    /organism="Brassica ole
/strain="TOL000DH3"
/db_xref="taxon:3712"
/clone="BOHBD63"
/clone_lib="BOHB"
/note="Vector: pHOS1; S
genomic DNA inserted in
a 126 c 162 g 2
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                                                                                          Score 308.8; DB 1
Pred. No. 4.1e-85;
0; Mismatches 182
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into pHOS1 using BstXI
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RESULT 7
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                                                                                                                                                                                                                                                                                                                          sequence.
BH448511
                                                                                                                                                                                               Town,C.D., Van Aken,S., Utterback,T. Whole genome shotgun sequencing of B Unpublished (2001) Other_GSSs: BOGOM52TR
                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                              BOGOM52TF BOGO
                                                                                                                                                                                         Contact: Chris Town
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                                                                                                                            S
     227
                                                                                                                primer:
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                                                                                                                                                301-838-0208
                                                                                                       sheared ends
                                                                                                                           from a doubled
/organism="Brassica ole
/strain="7010000137"
/db_xref="taxon:3712"
/clone="BOGOM52"
/clone="BOGOM52"
/note="Vector: pHOS1; S
genomic DNA inserted in
a 201 c 170 g
                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  GI:17634222
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                                                                         oleracea"
   into pHOS1 using Bst 244 t
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AUTHORS
TITLE
JOURNAL
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GAGAAGTGTCATTCATGGTGAAAGATGGCATTGTTTTGGGTCACAGGATATCA
                   GAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA 600
                                                                         CTTGCTAATCTGCAAGGTGCTGGAAAGATGTGAGGAGAAGAACTTGGTATTAAATTGG
                                                                                                                                            GACATTATGGAGGTTTTATGGACGATTTCTCAGTCTACGGTTCTTCATTTAGCGACTGC
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Whole genome shotgun unpublished (2001)
Other_GSSs: BOMPQ54TF Brassica oleracea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu Rosidae; eurosids_II; Brassicales; Brassicaceae; Bras Email: cdtown@tigr.org 1 (bases 1 to 768)
Town, C.D., Van Aken, S., Brassica oleracea. Medical Center 301-838-3523 301-838-0208 Chris BO_2_3_KB TR GI:18808105 Drive, Brassica sequencing haploid Utterback, T. 768 Rockville, oleracea provided õ. I. and Fraser, C.M. Brassica oleracea DNA genomic ð γģ 20850, linear clone Brassica. a; Tracheophyta; eudicots; GSS 20-FEB-2002 BOMPQ54, DNA

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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   Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Bras
1 (bases 1 to 814)
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                                                                                                                 sequence.
8H697068
                                                                                                                                       BH697068
BOMOT46TR
                                                                       Brassica oleracea.
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                                                                                                                                                                                                                           AAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTC 599
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/clone=11b="BO_2_3_KB"
/clone=1vector: pHOS1; Site_1: Bs
/note="Vector: pHOS1; Site_1: Bs
genomic DNA inserted into pHOS1
a 151 c 184 g 219 t
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/strain="TO1000DH3"
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1.3e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whole genome shotgun sequencing Unpublished (2001) Other_GSS: BOWOT46TF Contact: Chris Town
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AGCTGTTTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTG
                                                                                                                  GTGGAGAAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTTGGACCCCTCATTTGAC
                                                                                                                                                                  GGGTTATGTAATGCACCAGCCACATTTCAGAGGTGCATGCTGGCCATTTTTTTCAGACATG
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                                                  GACTGCCTTGCTAATCTGTGCAAGGTGCTGGAAAGATGTGAGGAGAAGAACTTGGTGCTA
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                                                                                                    ATTGAGGACATTATGGAGGTTTTTATGGACGATTTCTCAGTCTACGGTTCTTCATTTACC
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/note="Vector: PMOS1; Site_1: BstXI; 2-3 kb
/note="Vector: PMOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into PHOS1 using BstXI
a 178 c 195 g 217 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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RESULT 10 BH597975

LOCUS DEFINITION

BH597975 BOHGL95TR

BOHG

Brassica

805 bp oleracea

genomic

linear clone BOH

ear GSS BOHGL95,

15-DEC-2001

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REFERENCE
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DNA is from a doubled haploid
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/strain="T01000DH3"
/db_xref="Taxon:3712"
/clone="BOHGL95"
/clone=lib="BOHG"
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Tel: 301-838-3523
Fax: 301-838-0208
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Brassica oleracea
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BOHXT83TF BO_2_3_KB
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               AAGACGGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGGTTA
                                                      TGTTTTCTCGATGGTTACTCTGGGTTCTTTCAGATACCCATTCATCCAGACGACCAAGAG
                                                                                                           CACTTCCCACTTTCTTTCATTGACCAGATGCTGGAAAGACTAGCCAACCACCCCTACTAC
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                                                                                 TGTTTCTTGGATGGATACTCGGGATACAACCAGATCGCGGTAGACCCCCAGAGATCAGGAG
                                                                                                                                                                 ACGAAGGGTGGCATCACCGTCATCACAAATGAGAAAGCTGAGCTGATTCCTACCAGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 207 c 178 g 243 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHXT83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                            50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica
                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                            Score 304.4;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haploid
                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                181;
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AUTHORS
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KEYWORDS
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BH703456/c
                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids II; Brassicales; Brassicaceae; Bras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotun sequencing of Brassica oleraces Unpublished (2001) Other_GSSs: BOMGU48TF
                                                                                                                                                                                                                                                                                                                                                                                     Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH703456
BOMGU48TR BO_2_3_KB
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea.
                                                                                                             CGAATGTGTATCGACTATCGCAAGCTGAATGAAGCCACACGGAAGGACCATTTCCCCCTTA 198
                                                                            ATGACAGTGGTACGAGATGAGAGGAATGACTTGATACCAACACGAACTGTCACTGGTTGG
 AGAATGTGCATTGATTACCGAAAACTAAACTCCGCATCTAGAAAGGATCATTTCCCCATTA
                                                     ATCACTGTGATAAAAATGACAAGGATGAA--TGATACCAACAAGAACCATCACAGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAAGTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTCA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGAGGAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGAATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGCATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                               il: cdtown@tigr.org
is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                   primer: TR
                                                                                                                                                                                                                                              217
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Center
                                                                                                                                                                                                                                   /organism="Brassica oleracea"
/strain="T01000bH3"
/db_xref="taxon:3712"
/clone="BOMGU48"
/clone="BO_2_3_KB"
/clone="BO_2_3_KB"
/clone="BO_2_5_KB"
/clone="BO_2_5_KB"
/clone="BO_2_3_KB"
/clone="Voctor: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 163 c 144 g 219 t
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .743
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Brassica
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                                                                                                                                                                   Score 302.4; DB 1
Pred. No. 4.1e-83;
0; Mismatches 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oleracea
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                                                                                                                                                                                               DB 17;
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ae; Brassica.
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BOMGU48, DNA
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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KEYWORDS
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BH501651
LOCUS
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Query Match
Best Local Similarity 69.0
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BOGOH29TR
                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled !
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                             Town,C.D., Van Aken,S., Utterback,T. and Fra
Whole genome shotgun sequencing of Brassica
Unpublished (2001)
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                                                                                                                                                                                                              Class: sheared ends.
                                                                                                                                                                                                                                                                                                                     Contact:
                                                                                                                                                                                                                                                                                                                                   Other_GSSs: BOGOH29TF
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BH501651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATGTCCCTATGGTACCTTTGCATATCGAATGATGCCATTTGGTCTATGTAATGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGGTTATGTAATGCACCA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATACTCGGGATACAACCAGATCGCGGTAGACCCCCAGAGATCAGGAGAAGAGAGGGCCTTT 318
                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 796)
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                                                                            222
                                                                                                                                                                                                                                                                Medical Center Drive,
301-838-3523
301-838-0208
                                                                         /Clone_lib="BOGO"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
169 c 191 g 214 t
                                                                                                                                                                                                                                                                                                                    Chris Town
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                               /db_xref="taxon:3712"
/clone="BOGOH29"
                                                                                                                                                          /organism="Brassica
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOGO Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:17709748
                       50.4%;
         Score 302.4; DB:
Pred. No. 4.2e-83,
0; Mismatches 180
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           Indels
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                                  Length
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                                                                                                                                                                                                                                                                                           USA.
                                  796;
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        Gaps
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S

TTGGAGGCTGGGCTCATATACCCCCATCTCTGACAGCGCTTGGGTAAGCCCAGTACAGGTG

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BH443545/c
                                                                              FEATURES
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TITLE
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                                                                source
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)

other_GSSs: BOGGG29TF
Contact: Chris Town
                                                                                         Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                    BOGGG29TR BOGG
                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                            Brassica oleracea.
                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
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                                                                                                                                                                  Medical Center
301-838-3523
                                                                                                                                                   301-838-0208
    /organism-"brassica oleracea"
/strain-"TO1000H3"
/db_xref-"taxon:3712"
/clone="BOGGG29"
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                                                                         Location/Qualifiers
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Kozik'A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.

Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                                                                      Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                      BQ996483
QGG12P10.yg.abl QG_EFGHJ
QGG12P10, mRNA sequence.
BQ996483
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/note="Vector: pHOS1;
genomic DNA inserted;
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Pred. No. 5.6e-83;
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Best Local Similarity . 69.6%;
Matches 409; Conservative
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552 GTGTCATTTCATGGTTCGAGAGGGCATAGTCCTAGGCCACAAGATCTC 599
                                       481 AAACCTGACTGCGGTATTGCAAAAGTGTGTTCAACATAATCTTGTGCTAAATTGGGAAAA
                                                                             492 GAACCTAGAGAGGGTACTTCAGAGGTGCGAAGAGACTAACTTGGTACTGAATTGGGAAAA 551
                                                                                                                   312 GGCCTTTACATGCCCCTTTGGCGTCTTTGCTTACAGAAGGATGCCATTCGGGTTATGTAA 371
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singleton, see http://cgpdb.ucdavis.edu/ for details.
Plate: QGG12 row: P column: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asmundson Hall, UCD, I
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA '95616, USA
                                                                                                                                                        CATCGAGGTATTTATGGACGACTTCTCGGTTTTTGGACCCTCATTTGACAGCTGTTTGAG 491
                                                                                                                                                                                                TGCCCCAGCTACATTCCAAAGGTGCATGATGTCTATTTTTTCAGACATGGTTGAAAATTT 420
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TAG_LIB-QG_EFGHJ lettuce serricala
TAG_TISSUE-flowers environmental stress
TAG_SEQ-CGAATGCGGG"
112 c 162 g 220 t
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/lab_host="E.coli"
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/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGG12P10"
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541 ATGCCATTTATGGTAAAAGAGGTATTGTGTTGGGACACAAGGTTTC 588

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Search completed: June 20, 2003, 22:39:20 Job time : 2307.77 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Wright,D.A. and Voytas,D.F.
Direct Submission
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Wright,D.A. and Voytas,D.F.
Direct Submission
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/rpt_type=dispersed
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/gene="pol"
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                                                      CDS
                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                        Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MVAll
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/)
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/ggi-bin/sp.ggi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE).
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Arabidopsis thaliana genomic
AP001311 BA000014
AP001311.1 GI:7209747
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Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,

Birect Submission

Submitted (01-MAR-2000) Yasukazu Nakamura, Kazusa DNA Research

Submitted (01-MAR-2000) Yasukazu Nakamura, Kazusa DNA Research

Institute, Department of Plant Gene Research; 1532-3, Yana,

Kisarazu, Chiba 292-0812, Japan (E-mall:ynakamu@kazusa.or.jp,

Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and BAC clones
DNA Res. 7 (3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                         shorter because we remove overlaps between neighboring submissions. The 5' clone is T6J22 and the 3' clone is MSJ3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
                                                                                                                                                                                                                                                             This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0363099
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                                                 /clone_lib="Mitsui P1" complement(join(1709.
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1844 c
             2612. .2790))
/note="gene_id:MVA11.1
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                                                                                                         /db_xref="taxon:3702"
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                                                                                                                                               organism="Arabidopsis/strain="Columbia"
                                                                                                                                                                                                    Location/Qualifiers
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                                                    .1889,2017.
                                                                                                                                                                  thaliana"
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.2172,2316. .2444

	CDS		CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	CDS	
<pre>/pseudo /codon_start=1 /evidence=not_experimental</pre>	<pre>/product- yay-proceds polyproceds.inke complement(join(5326755857,5605157537)) /note="contains similarity to Pol-like peptide gene_id:MVA11.11"</pre>	/notce="gene_id:MVAll.10" /pseudo /pseudo /codon_start=1 /evidence=not_experimental /evidence=not_experimental	<pre>/pseudo /codon_start=1 /codon_start=1 /evidence=not_experimental complement(join(4733548223,4835949241,4941350566, 5070551104,5117451337,5148552374))</pre>	/pseudo /codon_start=1 /evidence=not_experimental /evidence=not_experimental complement(join(4479844894,4496845926,4601446233)) /note="gb AAF18631.1 gene_id:MVAI1.9 jene_id:MVAI1.9 jene_id:nvAI1.9	/codon_start=1 /evidence=not_experimental 43611. 43908 /note="gene_id:MYA11.8 unknown protein"	<pre>/pseudo /codon_start=1 /cvidence=not_experimental join(4044741304,4145842397,4258343109) /note="contains similarity to reverse transcriptase-gene_Id:MVA11.7"</pre>	/couch_start=1 /evidence=not_experimental /product="retroelement pol polyprotein" 3827538444 /note="gene_id:MVAll.6 unknown protein"	<pre>/codon_start=1 /evidence=not_experimental /product="En/Spm-like transposon protein-like" complement(2875230974) /note="gene_id:MVAll.5" /pseudo /pseudo</pre>	<pre>/codon_start=1 /evidence=not_experimental join(2343623872,2466324795,2488225169,2527425527, 2558025913) /note="gene_id:MVA11.4" /pseudo</pre>	/pseudo /codon_start=1 /evidence=not_experimental join(17769. 18220,19125. 19210,1932220811,2088621233, 2129821477,2155421653,2173422124,2220122517) /note="contains similarity to unknown protein gb AAF06087.1 gene_id:MVA11.3" /pseudo	/translation="MILETKTFFVWEVCQLGRCPIDLGGSQKCRRPDYPLALVCKHPN SGQTVWWSFGKKSTLKYGSGWDRVFWYRITAVYPBYPKLKILYQNIFKILENTQLLKEF EYVRVLDQVQVQSDLGSGFWVLKFRIRSDILKEWVRVRIGLEGGSSVQDFGFGEWYKV DPLVWNLESEMMEENRLVCLRDSMMYKEFASKVKEKLGVRAEDVVLEMSNKNPS" 17169. 17450 /note="contains similarity to replication protein Algene_id:mVall.2"	/codon_start=1 /evidence=not_experimental /protein_id="BAB0224.1" /db_xref="GI:9294327"
1 TGGCGCCGTTGTCGGGGA 18	Query Match 100.0%; Score 18; DB 8; Length 83339; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KKRKKVLIPRIII.SPODSKHPFTLERROPPVRMCYAMTVNKSOGOTINRVALYLPKPV PSHGQLYVALSRVTSPKGLTVLDTSKKKEGKYVTNIVYREVFNGLPAITGKKS" BASE COUNT 26491 a 15765 c 14391 g 26692 t ORIGIN	IKIGSMLAVYLSKVDI IWDEAPMAHRHTEEAVDRTIRDILSVGDEKALTKTIGGKTV LIGGDERQILPVIPQRTRQEETVSAAINRSYLWESCHKYLLSQNMRVQPEEIKFAEWIL QIGDGEAPRKTHGIDDDQEEDNII IDKNILLPETENPLEVLCQSVSPDFTNIEQDLEN LKGTAVLTPRNEFTVDEINDYLLSKVPGLAKEYFSADSIDQDEALTEEGFEMSYPMEYL NSLEFPGLPAHRLCLKVGVPIMLLRNLNQKEGLCNGTRLTVTHLGDKVLKAEILSDTT	/evidence=not_experimental /protein_id="BAB02227.1" /protein_id="BAB02227.1" /db_xref="GI:9294330" /translation="MEVLDSTNKNYTRRKQRENIGRIVNILPTAGDLYYLRILLNKVK /translation="MEVLDSTNKNYTRRKQRENIGRIVNILPTAGDLYYLRILLNKVK /db_xref="GI-YCTSTKYCGVVHESFKACHARGLLDGDKEWHDAMDEAAQWSTSYLLRSLFVLI GATSFDYLKTVGGVVHESFKACHARGLLDGDKEWHDAMDEAAQWSTSYLLRSLFVLI LIYCEVSEPLKLMSHCWESMADDVLRKQDGNVLNFPQLELRAKELEKYTLIEJETLLRQ HEKSLSDYPEMPQPEKSNGKNVMPVASSAIAALLLPGGRTAHSWFKIPINVHEDFICD	CDS join(7)345. 77871,7810679438) /note="contains similarity to unknown protein gb AAD25621.1 gene_id:myA11.17" /codon_start=1	/protein_id="BAB02226.1" /db_xref-"GI:9294329" /db_xref-"GI:9294329" /translation-"MCIGPRESQKTYEPKGPKKTQLKLQTLDFIFSNSIDAIQRTTKE /translation-"MCIGPRESQKTYEPKGPKKTQLKLQTLDFIFSNSIDAIQRTTKE KKSVSVTAPWSFPYFSSPEAQTSTVVGRLLRFWDARNIKKNDGQFMGIVLLLLDEKCSE IHAFIPAALASHFRQVLREGIIFNVSGFEVGRCTKLYKITDHPFLLRFLPATTIIEVS DVGPTIEREKFMLRNFDHLQALANINIELDDVGQITFVGGSNLNDFSTQRLVLRYK TDCGIVTYFCILGTPAALASHFRQVLREGIIFNVSGFEVGRVTTMAALASHFRQTATT	7680176930) /note="gb Asb25622.1 gene_id:MVA11.16 strong similarity to unknown protein" /codon_start=1 /evidence=not experimental	/note="gene_id:MVA11.15" /pseudo /pseudo /codon_start=1 /evidence=not_experimental /product="athila retroelement protein-like" /pioin(7574975952,7611076202,7628576558,7662976719,	/pseudo /codon_start=1 /evidence=not_experimental /product="retroelement polyprotein" /product="retroelement polyprotein" complement(join(7014170333,7073770900,7105471187, 7123371533,7158872066,7219972289,7234472573))	gene_1c:MVAII.13" /codon_start=1 /cviden.ce=not_experimental /protein_id="saB02225.1" /db_xref="gi:9294328" /translation="MGFKTLPSLPQKLMDHGLPFDTPAAAVERGTTPLLNYVFAELKD FATEIQSAGLVSFTPIIIGKVVELSPLWPHCMKESSCLVETQ" complement(6324666054) /note="gene_id:MVAII.14"	gene_id:MVA11.12" /pseudo /codon_start=1 /cvidence=not_experimenta1 /oin(59311. 59421,5952259671) /note="contains similarity to uroporphyrinogen III methyltransferase	complement(join(5756857707,5777957928,5805158165, 5827658305)) /note="contains similarity to disease resistance RPP5 like protein"

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31274

TGGCGCCGTTGTCGGGGA 31257

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COMMENT
FEATURES
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AUTHORS
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Submitted (27-FBB-2002) The Institute for Genomic Research, Submitted (27-FBB-2002) The Institute for Genomic Research, Senter Dr. Rockville, MD 20850, USA, cdtown@tigr.org Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598560.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
AC006413
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Town, C.D. and Kaul, S.
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Direct Submission
Submitted (09-MAR-2000) The Institute for Submitted MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAk, Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.-I., Carzera,A.J., Creasy,T.H., Buell,C.R., T. Nierman,W.C., Fraser,C.M. and Venter,J.C.
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1 (bases 1 to 106716)
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/note="PSK7.1; predicted by genscan"
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3087. .3184,3599. .3698,3901. .3995,4056. .>4317))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1. .5067)
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891. .1187
EEMVNTTKEGVENINCQDTCEAEDDDSGPEDDEVTCKENEEDEAGNDSLKEEDDEDDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="At2g06230"
/note="F5K7.2; pro
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/cultivar="Columbia"
                                                                                                                                                     /codon_start=1
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I IAREYFKOGK I EQFRO I LEEGSSSGKOLYDDAAS I CSRIDIDEYYADVK ERIAI LN
ALGAYY SYLCKTETKREKEEGE I SATRYYKRASRIDMEPSTWYGKGOLLAKGEI D
ALGAYY SYLCKTETKREKEEGE I SATRYYKRASRIDMEPSTWYGKGOLLAKGEI D
ALQAFR TYLDITAPDUVPALLGOASVEFROR TESELOLYKLGOLDKAROAFBYLOA
SGTGME I SSSYDIADCMROQIVLITII LELQLDPDNVEALLVALGIIMDLQANDSIGMRK
GMDENQQAFEI Y PYCASALNY LAANHFFETGGGYGLYCLTALAVTHGOTK SHSFYN
LARSYHSKODFEKAGMY XMAAI KETNINDHEEVF PY FYGLGOVOLKGELLKSSVERFEK
VLEVYPDNCETLKALGHLYTQLGQNEKALEYKMRKATKLDPRADAFVGLGELLISSDT
GAALDAFKAARTLMKKGGQEVFI EVLND I GALHFEREEFESALENFKEALGDGINISF
GAALDAFKAARTLMKKGGQEVFI EVLND I GALHFEREEFESALENFKEALGDGINISF
GAALDAFKAARTLMKKGGQETFI HILLESGHSYDV PMIKVTTLFULARLLEQIIKTEBA
ATEMYRLILFKYPGYI DAYLRLAASAKAQNNLPIA I ELVMENLAKULDKINPNALSLLGE
LELKNDDMVKAKETFRAANDATDGKDSY AL SELVENYFTQVOEBASGSVFLQMEDVW
VNLAHVYFAQGNEALTVKMYQNCLRKFFYNDDSQILLYLARHY EABONGECKETLLR
VLAHANDATAGKOS VALGENYFYNDSQILLYLARHY EABONGECKETLLR
VLAHAVYFAQGNEALTVKMYQNCLRKFFYNDDSQILLYLARHY EABONGECKETLLR
VLAHAVYFAGGNEALTVKMYQNCLRKFFYNDDSQILLYLARHY EABONGECKETLLR
VNLAHVYFAGGNEALTVKMYGNCLRKFFYNDDSQILLYLARHY EABONGECKETLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="(GA)n"
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/rpt_family="(GA)n"
/rpt_family="(GA)n"
/rotplement(14301. 15353)
/gene="Att206200"
/note="F5K7.4; predicted by genscan and grail; supported by cDNA: g1_16974616_gb_AY060586 1_"
complement()oin(<14301. 14687,14776. 14995,15089. \157
COMplement()
/rpt_family="GAA)n"
complement(16633..16694)
/rpt_family="AT_rich"
17318..26761
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join(<5036. 5176,5353. .5464,5508. .5702,5873. .5973,

5170. .6223,6446. .6653,6760. .6974,7189. .7276,7561. .7661,

7760. .7852,8195. .8263,8371. .8463,8538. .8798,9307. .9387,

9479. .9637,10062. .10157,10379. .10480,10559. .10666,

10766. .10990,11296. .11562,11666. .11737,11926. .12258,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="DNA sequence related
L12220)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIHLTPSNYTFRFDLGAVMQKSSSSTLQKKKRTADEVRSTVAEAENAVRVFTQLSAAS
DLHVHGFDSKKIQTHVQYCSHLLEAAKVHREAAEQEELQNRQRLEVARQAALAEEARR
KAEEQRKYQLEKRKQEEELRRLKQEEEKFQRIKEQWKSSTPGSNKRKDRVEDDDGESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(5036. 5176,5353. 5464,5508. 5702,5873. 5973,
6170. 6223,6446. 6653,6760. 6974,7189. 7276,7561. 7661,
7760. 7852,8195. 8263,8371. 8463,8538. 8798,9307. 9387,
9479. 9637,10062. .10157,10379. .10480,10559. .10666,
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DSKYCERHMHRGKNRASSRKEPPTQFTPNLFLDSSSRRRRSGYMDDFFSIEPSGSIKS
CSGSAMEDNDDGSCRGINNEEKQPDRHCFILGTDLRTRERPLMLEEKLKQRDHDNEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(14369. .14687,14776.
/gene="At2g06200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POKEKEESNGEAGDPNMEEEEEEEEAN" complement(12724. .12818)
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EYHEKYLLDSLLEDDYDDDLDLIDIYIDNWKGRLFYEKKKIWWKGMFPELDAVVASIN
SLTQMMTKGFEETRDKIDAIDGRYKSIELFVADLKEKKHGKQTEEESQHGKQTEEEVF
                                                                                                                                                                                                                                QGSKRFYRFLDEWPSSKSSVSTSLFI"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="expressed protein"
/protein_id="AAD19769.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAEEPVDDDAHDLLAAAGLEDPDVDDDEVPTSGVRRRRALSSSDEEGELMEESHPNSS
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/protein_id="AAM15237.1"
/db_xref="Gi:20197768"
/translation="MASVYIPVQNSEEEVRVVLDQLPRDASDILDILKAEQAPLDLWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At2g06210"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/note="Putative Ty3-type retrotransposon,

structure:

long

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                                      AP004483/c
                                                             RESULT
    DEFINITION
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                                                                                                                      49148
  Lotus japonicus
                                                                                                                                      1 TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                               18;
                      AP004483
                                                                                                                                                                                                                   Similarity
                                                                                                                      TGGCGCCGTTGTCGGGGA 49131
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                      complement(join(23597. .23821,24081.
25986. .26243,26258. .26464))
/gene="AL2g06170"
                                                                                                                                                                                                                                                                                                                             complement(join(<23597.
25986. .26243,26258. .>
/gene="At2906170"
                                                                                                                                                                                                                                                                                                                                                                                                            complement(23597. .26464)
/gene="At2g06170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRRSSGRSQGRGRGSRGRGPNRSQEVRQTSNLGGGSAGNRPFHWSYTHDRDHPIIEDK
AGLANLLRHIIGRNCQVPGDCCYKQVCCSLRATSKQGSFGERARREDDHLGVDSERE
VRSGARGIVPGMLRLKMELSTSKDLEKGYAEKIKIMEQEFFGLEADKQMARNQIHRL
EKKDELSKRVLDLTSIAQGVNRAVHDAKVELAASYSKLLSGIKDKWYAKKETTVLESQ
AAEVESNLALIDQIVKAAVDLTVEKPRFQAEIDDVEARCTLKEVSDFTLSKLDIPEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminal repeat B (LTRB)"
complement(17533 .18380)
/gene="At2g06190"
/note="F5K7.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKNQRNHFFRDETLSVDPSSKLSNRLATFNRDRNVTALPIDPADPVIALPAAQPDPLE
EVPQLYFRPSAYFQKKNEVTKSSCSTSQCGTSARAGDLSAVVAAARTSLAASHTQAST
SHPSLPAANARPLLARRARLLPVYRLTAELIVLDQEVAPSREEEVKPLAANPEAAVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKPKKKKAPKOKGSLPMTNNDLEVLDSGGGDYDTPKVAAVTQERAGGVGLCLRQFLRE
MWAVLPDSGVHPRDALLPRLRLSSNVSKFRPPRAGVIYPGLRGEQRIRLPRPAAALSG
QDQRQERPRDVLHKCSSWISDPRWSEGLSGYKLASQILLLQGGHHSVGDFDPARITRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MTRLFSAPHLTAQIRRGEEISTISKIYVMMASLNNFPHLHSISR
QLTRLPSDLDDSQNKSNHSYGDDDSSSKMRSAASSRQEPRRVITLGGMGPIRRPSTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFFKEVVRLHGVPKSITSDRDTKFLSHFWSTLWRMFGTALNRSSTPHTQIDGQTEVTN
RTLGNMVRSICGDNPKQWDLALPQIEFAYNSVVHVVDLVKLPKALGASAETMAEEILV
VKEVVKAKLEATGKKNKVAADKRRRFKVFKEGDDVMVLLRKGRFAVGTYNKVKPRKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative Ty3-gypsy-like retroelement pol
polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(17533. .17932,17938. .18380))
/gene="At2g06190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(<17533. .17932,17938. .>18380))
/gene="At2g06190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMLVVRPMNVDEQGTPIGLDEFGSNKDTFPRGLEEDPGTVFATPAGGSKECHG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFKVLRKINDNAYVVALPKSMNISNTFNVADIHEYHADGVLYPEENLRTSSSEVEETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD19756.1"
/db_xref="GI:4388718"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     terminal repeat A (LTRA), putative Ty3-type pol
polyprotein-1, putative Ty3-type pol polyprotein-2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(<19174. .19325,19483. .19702,19717. .20174,20300. .20483,
20634. .20843,20930. .21110,21129. .21302,21427. .21586,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="At2g06180"
/note="F5K7.6"
                                                                                                                                                                                                                   100.0%;
122116 bp DNA linear PLN 14-DEC-2001 genomic DNA, chromosome 1, clone:LjT13004, TM0016,
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                                                                                                                                                                                               0,
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                                                                                                                                                                                           Score 18; DB b,
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                     .>26464))
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.21110,21129. .21302,21427. .21586
                                                                                                                                                                                                                                                                                                                                                                          .23821,24081.
                                                                                                                                                                                                                                 Length 106716;
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KEYWORDS
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                    COMMENT
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Best Local
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                                                                                                                                                                                                                                                      Sasaki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   AP003054.2
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predicted
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52966 TGGCGCCGTTGTCGGGGA 52949
                       Direct Submission
Submitted (20-DEC-2000) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL.http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Mar 16, 2001 this sequence version replaced gi:11967926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148246 bp DNA linear Oryza sativa (japonica cultivar-group) genomic DNA, ADDOCCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
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                                                                                                                                                                                                                                                Published Only in Database (2000) 2 (bases 1 to 148246)
                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lotus japonicus
                                                                                                                                                                                                                              Sasaki, T., Matsumoto, T. and Yamamoto, K
                                                                                                                                                                                                                                                                                                                    clone: P0436D06
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone: P0436D06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lotus japonicus DNA, clone_lib:LjT library clone:LjT13004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP004483.1 GI:17736850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="LjT13004"
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, 23562 c 23033 g 38363 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:13359042
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                                                                                                                                                                                                                                                                                                                                                                                                                            Magnoliophyta; Liliopsida; Oryzeae; Oryza.
sequence version replaced gi:11967926. from the integrated results of the following:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 122116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poales;
                                                                                                                                                                                                                                                                                                                                               chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 1,
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FEATURES
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The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0436D06 clone has an overlap with P0507H06 (DDBJ.AP003144) clone at 5' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CWFMVYKVGMGNAGAALSVSICDWVEVTVLGLYIVLSPSCEKTRAPLTWEAFSGIGSF
IRLAVPSALMILEWWSYELLVLLSGILPHALETSVLSISGGSVSIELGAGNPEGA
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IGQQPEIASEVGKYALWLIPGLFAFTVAQCLSKFLQTQSLIFPMYLSSSITLALFIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYHLNLKQKVITIAALAPKRPPSLRKPAVIVPVFDNRSAPVVAKQGKDWKEAVVVQHR RHPSHSTRATRGQDIWYRGSQSQYRIKNHSWAISLDFVETIDKSTKSG" complement(join(19066 .19338,19622. .19876,20096 .20179,
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/gene="P0436D06.4"
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VDFDLKSSLITMAQASPFCGKPNEDADAHL"
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/gene="P0436D06.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATOVTLLSIITAMTNWRKMVGSFFPFLLHKVLSVQAVSKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to Arabidopsis thaliana Chromosome 1, F9L1.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(19066. .19338,19622.
21788. .22330,25632. .25949))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB33265.1"
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join(1618. .1860,2195. .2404)
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/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                /gene="P0436D06.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-"hypothetical protein"
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                                                                                                                                                                                                                                                                                             'note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                  .31494)
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55967..56189)
/gene="P0436D06.8"
join(53501..53821,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38066. .38853
/note="5' LTR"
complement(38856.
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KEASSSDSADKEVQPEKTMPQEHCDTRLLSFPQRSRKPSVDEQLARFVEVIQKIHINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQCSMDKVRVESVEYSSGRSGATQDGQPVEVHAEFPREGNNDAQEPLLEDAGKTTHTG
QEARAANSEEAALRTKANEGVEGEAKDARSITSRDGMRRRLSRLFKGSGSSSSHHDES
STRSSAVVSMEDAKAPRRLLNGTDIDHVNDRERQAYYMLSDWEYAHTREYSPELLKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(38856. .43616)
/gene="P0436D06.6"
/note="probably inactive due to stop codon in pseudogene, gag-pol polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0436D06.6"
complemen+/^^~
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complement(36243. .37369)
/note="3' LTR"
                                                                                                                                                                                                   join(57860. 57947,57977. 58160,58266. 58488,58712. 58743,
59094. 59199,59234. 59612,59620. 59747,62210. 62476,
62757. 63233,63954. 64091)
/gene="p0436D06.9"
                                                                                                                                                                                                                                                                                                                        join(57860...57947,57977...58160,58266...58488,58712...58743,59094...59199,59234...59612,59620...59747,62210...62476,62757...63233,63954...64091)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Juin(35422. .35884,35924. .36131,36163.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(52237. .53379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pseudogene, retrovirus-related pol polyprotein from retrotransposon 17.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYHLYNYRELTIPLQTIEESRAGGAYRETRNMARNERKSSSSTPVQISSGVPPSPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(46544..48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oin(35422. .35884,35924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="probably inactive due to stop codon in CDS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene-"P0436D06.
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                                                                                                                                                                             'note="hypothetical protein"
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                AL Published Only in Database (2001)

22 (bases 1 to 189744)

23 (bases 1 to 189744)

24 (bases 1 to 189744)

25 Sasaki, T., Matsumoto, T. and Yamamoto, K.

26 Sincert Submission

27 Submitted (02-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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189744 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 6
*** SEQUENCING IN PROGRESS ***, in ordered pieces.
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18; Conserv
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the finished sequence as soon as it is available and
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complement()oin(66849. .66972,67147. .67435,67625.
68423. .68608,71933. .71987,72830. .72928))
/gene="P0435006.11"
complement()oin(66849. .66972,67147. .67435,67625.
68423. .68608,71933. .71987,72830. .72928))
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VRDQTTECAVCRGAFDTAELLRVLSQCQHAFHGCIDVWLMTHSACLVCRRSADGALL
RVPGNORFLAMYERQRGRGSAATGADGSVHRGHBERLERGGRRSRVGKTLPIEKPAVPV
PPTFKTMADKTLREFAAPSAENVAIGPQINMGDVDFDLKSSLITMAQASPFCGKPNED
ANAHLQQFPEICCTYTIKGNEYNGLIPMSRDHLDAAAGGAFFSKTWQGAVDLIEKLVS
NMGWSERRLQTRQRGMTTVKEMELFAAKLDLLMKCLDDHDKRPQGTVLALDSHVTCEV
YGKAPSSFWTHMLFWRSTATTRVILGMTARKPVRRRCIWATTITGTVHKEVRGGTSHAR
TIKELTDILANTLIPMPSWYFEKFQTAELLTTVRHDHTTGLNTEEYPP"
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/db_xref="GI:13359050"
/translation="MyVDFTDLMKVCPKDHFPLARIDQLVDSMAGCELLSFLDAYSGY
HQNSMAKEDEEKTTFITPFGVFFYTRMPFGLISVGNTYQREIQGALGDQIGWNVETYI
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/gene="P0436D06.10"
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complement/66222
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Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                            2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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. Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-MAY-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannov
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2 (bases 1 to 194640)
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                                                                                                                                   /db_xref="taxon:39947"
/chromosome="7"
                                                                                                                                                                        /organism="Oryza sativa/cultivar="Nipponbare"
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/chromosome="6"
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                  Score 18; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                              gene
                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei)F., Wing,R.A. and Wise,R.P.

Direct Submission
Submitted (03-0CT-2001) Plant Pathology and Interdepartmental
Genetics, USDA-ARS/Iowa State University, 351 Bessey Hall, Am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wei,F., Wing,R.A. and Wise,R.P. Genome dynamics and evolution of the Mla resistance locus in barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare Mla locus, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Cell 14 (8),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF427791.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50011-1020,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF427791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 261265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 261265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Stowaway.1; miniature inverted transposable
element-like sequence; type Stowaway"
/rpt_family="MITE"
                                         /note-"predicted by GenScan; similar to barley glycine-rich RNA binding protein, CAA88558, pathogen
                                                                                                                                                                                     element-like sequence;
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LTGLKIFWTCYVLKNEYERVATMRLRFLASEKRRPDQFTVLVRNIPPDDDESVSELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental complement(join(<476. .581 2585. .2898)) /gene="711N16.16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="predicted by GenScan; similar to Arabidopsis
predicted proteins AAD36947 and BAB02357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_type=dispersed
complement(<476. .2898)
/gene="711N16.16"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/chromosome="5"
                                                                                                                                                                                                                                                                         HEELVNHPDHYLKHQV"
                   response protein"
                                                                                  /gene="711N16.15"
)oin(4045. .4080,4158. .4466)
/gene="711N16.15"
                                                                                                                                                                                                           /note="Stowaway.2; miniature inverted transposable
element-like sequence; type Stowaway"
                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hv711N16.16"
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/clone_lib="HV_MBa-Library, Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Socation/Qualifiers
                                                                                                                                                                rpt_type=dispersed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:20513849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261265 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .581,1029. .1164,1898. .2044,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (powdery mildew)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLN 12-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ames,
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                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tRNA
                                                                                    repeat_region
29590 29746 notes inverted transposable element-like sequence; Type Hormitel levidence=not_experimental /rpt_family="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(15373. .21468)
/gene="Bpm"
                                                                                                                                                                                                             /evidence=not_experimental
complement(25299. .25490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                     /pseudo
/evidence=not_experimental
                                                                                                                                                /note="predicted by
naturase; truncated
                                                                                                                                                   maturase;
                                                                                                                                                                                                                                                                            /note="predicted by Blastx
naturase; truncated gene"
                                                                                                                                                                                                                                                                                                                                        complement(22721. .22903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAM22812.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="BPM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3GGGGGLAQGGG"
                                                                                                                                                                                            /gene="Bmta
                                                                                                                                                                                                                                                                                                                   /gene="Bmtb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="711N16.14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="tRNA-Ser"
                                                                                                                                                Blastx
d gene"
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SPRIGARSPGGTLSSRÖNLAGASNYLGYNGVGSPTGASSLQMPIDPLYLQYLAAQVAA
SYDDPFMASGHLGSSYMDLLGPQKGCLSPLLOSQKNYGCYGNLGFGLGYAGSPLTSPV
LPSSPVASGSPLRHGERSMRFASGMRNEGGSFGSWSPDMVGKMEGNLMPSLLEEFKSN
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GGGGEVLLDDELRADPAYQSYYYSNAHLNPRLPPPLLSKEDWRSASTASAPPPPPPGS
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SKFIAVHTSCVHELPLHTLQEDSNQRDVDDRQSANHSRNDFLDSSGMQYALHRUTGAM
GGLQRESNEQTLADIRNNELSSHASASPDPELVRRVPSPCLPPLGVKVGAYDKKSNGG
SSSFRRSSSAVGEPDDLVAALSGMNLSSSRAGNGQAMDQSKLYQDVDNANRYLFDRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"puf family; predicted by GenScan; similar to Arabidopsis putative pumilio/Mpt5 family RNA-binding protein AAC95220 with barley matches ESTes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(15373. .15413,15516. .15690,15778. .15972, 16919. .17029,17133. .17345,17868. .17975,18057. .18198, 18994. .20019,20053. .20234,20869. .21007,21065. .21468))/gene="Bpm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hv711N16.15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence-not_experimental
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product="HV71N16:14"
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RTPPMRHRTSASHTAKTVSWSPPQVPDSSTTRDCVKLSSASEMSPSVAATRVSKEEPD
                                                                                                                                             ETCDDQQREMILTRIKAHLNTLKKYTYGKHIVARVEKLVAAGEKRQGLQPACTAA'
                                                                                                                                                                                            LEHCDDPTTQQIMMDEILQSVCLLAQDQYGNYVVQHVLEHGKPHERTAIIDKLIGQIV
QMSQQKFASNVIEKCLAFGNPVERQILIGEMLESTTESEPLEVMMKDQFANYVVQKVL
                                                                                                                                                                                                                                                                                               ELDGHIMRCVRDQNGNHVIQKCIECIPQDIIQFIVSTFYGQVVLLSTHPYGCRVIQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQTSGNQQHSFMKRPEQGHFRAPEGYSANSANSSMMRNQMNAGNFTSSDNSSVGSGYA
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search; similar to Poaceae
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similar

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Poaceae

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RESULT 10
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                             LOCUS
    DEFINITION
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                                                                                                                                               256409
                                                                                                                                                                                                                                                                    Local
APO02458 67517 bp Arabidopsis thaliana genomic DNA,
                                                                                                                                                                                            μ
                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                             TGGCGCCGTTGTCGGGGA 256392
                                                                                                                                                                                               TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                /rpt_type=dispersed 49126. .49163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           element-like sequence; type Stowaway"
/rpt_family="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="partial; part of polyprotein and 3' untranscribed
or translated region deleted, the LTRs are intact"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="coding region not determined; predicted by BLASTn
and EST search; barley DCINA-induced gene; similar to th
sequence deposited in GenBank Accession Number AJ250665"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_type=dispersed
<29965. .>30140
/gene="Bdi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Hormites3.1; miniature inverted element-like sequence; type Hormite3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transposon="Copia/Gypsy-like retrotransposon BARE-1"
47953. .47957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRRVGRQASLGPPDTTDLSGYDAAVGCRVRMDGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37785. .39765
/gene="711N16.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPRRPPTLSCSVAIRTARVVPLGRSCWEDFGSQAEVMGGHDEVK
LVQFKPAAIDCSVQRPFPAIVVHLQMLHGVARVYRRRRSRGGDIGARLYDGVVVVVVD
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/rpt_family="HORPIA-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/rpt_family="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence; type Hormite2"
                                                                                                                                                                                                                                                                                                                                          /note="Hormites3.2; miniature inverted transposable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Stowaway.3; miniature inverted transposable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted by GenScan; function unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jóin(37785. .37972,38394. .38577,39727. .39765)
/gene="711N16.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type=direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposon="Ac-like transposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"incomplete ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="miniature inverted transposable element-like
                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/rpt_family="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="BARE-1 SoloLTR-1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="5-bp insertion signature (BARE-1 SoloLTR-1.2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAM22813.1"
/db_xref="GI:20513852"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transposon="Copia/Tyl-like retrotransposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insertion signature (BARE-1 SoloLTR-1.2)"
                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                    2e+02;
  chromosome 3, BAC clone:T22C2
                                                                                                                                                                                                                                                                                          DB 8;
                           DNA
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                     Length 261265;
                                                                                                                                                                                                                                           Indels
                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transposable
                        PLN 27-DEC-2000
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, pl
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=T22C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute, Department of Plant Gene Research; 1532-3, Yana
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-JUN-2000) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP002458 BA000014
AP002458.1 GI:83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Structural Analysis of Arabidopsis thaliana Chromosome 3. III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:TAMU BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 67517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r because we remove overlaps between neighboring submissions. clone is T22B15 and the 3' clone is T1013.
                      /evidence=not_experimental complement(1423. .1696) /product="(+)-delta-cadinene synthase (d-cadinene synthase) like"
                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
complement(423. .758)
/product="(+)-delta-cadinene synthase (d-cadinene
                                                                                                                                                                                                                                                                                                              /note="CDS is reported in
gene_id:T22B15.28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="CDS is reported
gene_id:T22B15.28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(32. .199)
/product="(+)-delta-cadinene synthase (d-cadinene
                                                                                                                                                                                                                complement(909. .1318)
/product="(+)-delta-cadinene synthase (d-cadinene
                                                                                                                                                                                                                                                                                                                                                             synthase) like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthase) like"
/note="CDS is reported in Acc# AP002062
                                                                                                                                          /note="CDS is reported in
yene_id:T22B15.28"
                                                                                                                                                                                               synthase) like"
                                                                                                                                                                                                                                           /evidence=not_experimental
complement(909. .1318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="TAMU BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana"
                                                                                                                                                                      Acc#
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CDS
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product="(+)-delta-cadinene synthase (d-cadinene
synthase) like"
/note="CDS is reported in Acc# AP002062
gene_id:T22B15.28"
                                                                                                                                                                           complement(join(34053. .35108,35292. .35906))
/note="contains similarity to non-LTR retroelement reverse
                                                                                                                                                                                                                   /translation="MGADIVADGLTDRPPDRLADEPAEGLSDRLPEGLSEEPADELVD
KLNLTKEPHDVLEDFLLFIFTLMKTTRHLGAAEMTHILFTHPKPREKNLSLIGGSLAF
SLKIEYSPLDPVCLLTLEDLSKT"
                                                                                                                                                                                                                                                                                                                                                         gene_id:T22C2.7
similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                               /evidence-not_experimental 33467. .33844 /note="emb|CAB81790.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
complement(30211. .31032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"contains similarity to unknown protein emb|CAB77997.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONGGEEQADDDDDEEHPQTYHN"

complement(join(15703. .16226,16332.

17792. .17980,18269. .18867,18953. ..

20974. .21359))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPRRQNLRSIVASMPRIWGQSGLVHGRIMEGRQEHFIFTLEESLETVLRRGPWAFNDW
MILLQRWEPQIPLFPFIPFWVQIRGIPFQFLNRGVVEHIGRALGQVLDTDENVEVVAR
MDFARVLLHWDITHPLRFQRHFQFTAGVNTLLRFRYERLRGFCEVCGMLTHDFGACLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(11186. .11911)
/note="gene_id:T22C2.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental complement(join(3258. .7313,8240. .8346,8681. /note="gene_id:T22C2.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene_1d:T22B15.28"
                                                                                                                                        gene_1d:T22C2.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
/product="Tall non-LTR retroelement protein-like"
/protein_id="BAA97081.1"
/db_xref="GI:8777563"
/translation="MADNLRRAVQDINLGVDDIPFALPEDIVNHAVAENRFILFGRPV
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/cvidence=not_experimental
/oin(35982 . 36259,36422. .37100)
/note="gene_id:T22C2.9
                                                                                                                                                                                                                                                                             /evidence-not_experimental
/protein_id="BAA97082.1"
/db_xref="GI:8777564"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/product="helicase-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="non-LTR retroelement
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                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="contains similarity to retroelement pol
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unknown
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                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                             RESULT 11
AF028277
                                                                                                                   DEFINITION ACCESSION
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                                                                                                                                                             Pocus
                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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17; Conserv
                                                                                                 AF028277.1
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                                                                                                 GI:4581593
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43810 TGGCGCCGTTGTCGGGG 43826
Hordeum chilense.
Hordeum chilense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                      Hordeum chilense RAPD marker AF028277
                                                                                                                                                                                                                                                                                                                                                               TGCCCCCGTTGTCGGGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSSDNFFTFASFEDIKSGSLDTNICVGTKTYRNVLVYKYYRRNQ NDEGPPDNEWNEIFFDIENVEGDKLTCRLKAYANDFFDNWRHCVDKIIICVMRPAKL KVDGGLASODGARLYESFIEPSMCRS"

join(48668. 48804,48803. 49148,49230. 49299,49414. 49567,49794. 49928,50041. 50200,50258. 50423,50538. 50697,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MALDTASNGEFMTKTETEATKLIENLAGSNSNHNVDYDRSNRGG
GGESKGPAELAKVEQLMRRDORSVNRGCEDSSKGMVHGEFSGDGSEDLQAEINEVNGS
TNVENPODDYVEPTQAGSGGOKEQPVEFQNKGMYGGPOPPAGTGHASSEGLDAEINEVNG
QVLEDQKKNAADINVKVDSMYNDLNGKFATLSSHVKTLENQVSQIVSASMRPDGTHS
GKYKFRGKEQCYAIMIQEELAEIVVAKQUETNVVVETLVEDKIVEDDEPLSVEPPPY
VPKLFFPGRERQIQRKEYARFDEIMKQLYVRLFFIQDLHVPSYRSYKKYLISNKRS
IEBGVKLISKGEHAQLVESQNKQQKEAQUTNVFTLYDENTUSTAIPATIPKLG
ITNTKPSRISLILADBSVQFPMGLAENVHARVGNFYIPTNFVLCHAUEPHDDLNLGR
ITNTKPSRISLILADBSVQFPMGLAENVHARVGNFYIPTNFVLCHAUEPHDDLNLGR
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AHVILIPLQRVEDTIEYKVQCKGTSKPFSKARSILTSEWKEKGRKAVKRVVGKVLRMK
LTDWRFCEGASSRTRVH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/product="replication prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
join(51608. .51745,51834. .52098,52211. .52313,52391.
/note="gene_id:T22C2.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/protein_id="BAA97084.1"
/db_xref="GI:8777566"
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/note="gene_id:T22C2.12
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/product-"retroelement pol
join(44238. .44539,44606.
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/pseudo
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3. 7.2e+02;
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.45477,45594. .45890,45945.
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        Brassica nigra
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1732)
Bhanot,R., Srivastavs,P.S., Delseny,M., This,P., Singh Negi,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 bp
Sequence 13 from Patent WO0055325.
AX059280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (06-OCT-1997) Agronomia y Mejora Vegetal, Instituto de
Agricultura Sostenible (IAS), Avda. Menendez Pidal (Alameda del
Obispo), Cordoba 14080, Spain
                                                                                                    X89901.1 GI:927389
Transfer-RNA.
                                                                                                                                                                                                                                                                            . Similarity
17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thale cress.
Arabidopsis thaliana
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17; Conser
                                                                                                                             B.nigra DNA for tRNA like X89901
                                                                                                                                                                                                                                                                                                                                                                                                           Preuss,D., Copenhaver,G. and Keith,K. Plant chromosome compositions and methods Patent: WO 0055325-A 13 21-SEP-2000;
The University of Chicago (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 537)
Hernandez, P., Martin, A. and Dorado, G.
                                                                                     black mustard.
                                                                                                                                                      BNDNATRNA
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Lakshmikumaran,M.
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/db_xref="taxon:15565"
/clone="IAS-pHcR9"
/83 c 111 g
                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
135 c 115 g 196 t
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1. .687
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Pred. No. 2.
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17; Conserv
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Direct Submission
Submitted (24-JUL-1995) M.S. Lakshmikumaran, Tata Enery Research
Inst., Darbari Seth Block, Habitat Place, Lodhi Road, New Delhi,
                                                                                                                                                                                                                                                                    Ivashuta, S. and Naumkina, M.

Direct Submission
Submitted (23-007-2001) Graduate School of Agriculture,
Submitted, North-9 West-9, Kita-ku, Sapporo, Hokkaido (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago sativa LTR retroelement MCIRE hypothetical complete cds. AF439379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New family of dispersed repeats from Brassica nigra; characterization and localization Theor. Appl. Genet. 930, 1123-1129 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                 Genotype-dependent transcriptional activation of novel repetitive elements during cold acclimation of alfalfa (Medicago sativa L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Kapila, R., Negi, M.S., This, P., Delseny, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Shimamoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 4717)
Ivashuta,S., Naumkina,M., Gau,M., Uchiyama,K., Isobe,S., Mizukam,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago sativa
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                                                                                                      /organism-"Medicago sativa"
/db_xref="taxon:3879"
/db_ne="pMcire7"
/clone="pMcire7"
/transposon="LTR retroelement MCIRE"
/note="putative LTR retroelement"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="transfer RNA like molecule"
1268. 1732
/note="homology to Bn4 (X67835)"
406 c 339 g 446 t
                                                                                      1586.
/evidence=not_experimental
/product="hypothetical pro
                                                                                                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:3710"
                                           /codon_start=1
                                                               /note="cold-inducible"
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060-8589,
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Thes 17; Conserve
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Search completed: June 20, 2003, 23:23:59 Job time: 78.956 secs
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Best Local Similarity
Matches 17; Conserv
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MEDLINE
PUBMED
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Direct Submission
Submitted (09-JAN-1992) P. Langridge, University of Adelaide,
Centre for Cereal Blotechnology, Waite Agricultural Res Inst, Glen
Osmond, South Australia 5064, AUSTRALIA
2 (bases 1 to 6676)
2 (bases 1 to 6676)
Rogowsky,P.M., Liu,J.Y., Manning,S., Taylor,C. and Langridge,P.
Structural heterogeneity in the R173 family of rye-specific
                                                              repetitive DNA sequences
Plant Mol. Biol. 20 (1), 95-102 (1992)
92385773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ScR1731 6676 bp DNA linear P S.cereale DNA for dispersed repeat sequence (R173-1).
                                                                                                                                                                                                                                                                                                                                                                                                        See also X64100-3.
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ERLLSKEEIFEQKGKKVSKAEIDRVIDEICALFKSKLRRTWTSHQLYLKFMEFLPKRR
VSKDDVLSVSFWPP"
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/note="long terminal repeat 2"
a 1374 c 1405 g 2222 t
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transloction from Rye"
                                                                                                                                                                                                                                                                            /db_xref="taxon:4550"
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/clone_1ib="lambda EMBL3"
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Pred. No. 1.9e+03;
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Result
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Maximum DB seq length: 200000000
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16.4
16.4
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2: /SIDS2/gcgdata/gc
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18
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                                                                                                            AAZ35254
AAZ35271
AAZ35275
AAZ35261
                                                                                           AAF22107
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                Arabidopsis thalia
Mycobacterium tube
Arabidopsis thalia
Mycobacterium tube
                                                                                                                                                                                                                          Description
                                                                                                         Soybean retroeleme
Soybean retroeleme
Plant generic retr
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ABA63912 ABA31089 AAK12418 AAK38131 AAI18911 AAI44032	ABN79856 AAZ35424 ABA76135 ABA40687 AAK24801 AAK24801 AAK50798 AAI27820 AAI27820 AAI27820 AAI27820 AAI27820 AAI39778 AAS29778 ABS24287 AAS29778 ABS24287 AAS2973	
Human foetal liver Probe #9555 for ge Human brain expres Human bone marrow Probe #8844 for ge Probe #12718 used	retry retry foet foet foet	bacterium tubacterium tubacterium tubacterium tunucleotide funucleotide fulum venenatu short-chain human codin human codin secreted prophila melano the virus nuc secreted protide sequentied HIV protied HIV prot

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ALIGNMENTS

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RESULT 1
AAZ35254
29-MAY-1998;
28-MAY-1999;
                                                                                                       02-DEC-1999.
                                                                                                                                      Glycine max.
                                                                                                                                                                           Plant retroelement primer binding site version
                                                                                                                                                                                                          AAZ35254;
                                                                                                                                                                                                                        AAZ35254 standard;
                                                                                        28-MAY-1999;
                                                                                                                      WO9960842-A2
                                                                                                                                                    primer binding site; soybean; ss.
                                                                                                                                                            Retroelement; retrovirus; transgenic plant; gene transfer;
                                                                                                                                                                                           27-MAR-2000
                                          (WRIG/) WRIGHT D A. (VOYT/) VOYTAS D F.
                                                                                                                                                                                          (first entry)
                                                                98US-0087125.
99US-0087125.
                                                                                        99WO-US11858
                                                                                                                                                                                                                          DNA;
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4403765

AAF22303 AAI99683

Mycobacterium

New nucleic acid molecules for imparting agronomically significant

WPI; 2000-105586/09.

Wright DA, Voytas DF;

AAH51978

characters

to plants, especially soybean

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RESULT 2
AAZ35271
ID AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
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COL
XX CALy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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  This is the nucleotide sequence of the Calypso 1-1 retroelement of soybean. It was identified by screening of a soybean lambda library using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AAZ35271-73) and Calypso 2-1 and 2-2 (see AAZ35274-75). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calypso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 1 A; 4 C; 9 G; 4 T; 0 other;
                                                                                                                                                                                                                                New nucleic acid molecules for imparting agronomically significant characters to plants, especially soybean
                                                                                                                                                                                                                                                                                                                        WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                                                                                                                Wright DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Retroelement; retrovirus; transgenic plant; gene transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean retroelement Calypso 1-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ35271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ35271 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (WRIG/) WRIGHT D A. (VOYT/) VOYTAS D F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGGCGCCGTTGTCGGGGA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                                                                                                · Voytas DF
                                                                                                                                                                             Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          soybean; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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99US-0087125
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                                                                                                                                                                           118pp;
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Pred. No. 34;
                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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RESULT 3
AAZ35275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc retroelements include gag, pol, env and primer binding site cc sequences that can be used in constructs of the invention. The c invention provides molecular tools in the form of retroelements and cretroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line c which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has c retroelement sequences that allow for replication and integration. C claimed isolated nucleic acid molecules comprise a nucleic acid c sequence selected from a retroelement primer binding site, envelope, integrase, reverse transcriptase, protease or MASe-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that c particles are used to transfer the nucleic acids into plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                       This is the nucleotide sequence of the Calypso 2-2 retroelement of soybean. It was identified by screening of a soybean lambda library using a reverse transcriptase probe. 2 Groups of soybean retroelements were identified, i.e. Calypso 1-1, 1-2 and 1-3 (see AA35271-73) and Calypso 2-1 and 2-2 (see AA35274-75). The retroelements include gag, pol, env and primer binding site sequences that can be used in constructs of the invention. The invention provides molecular tools in the form of retroelements and invention provides molecular tools in the form of retroelements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calypso 2-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ35275 standard; DNA; 10482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9829 BP; 2948 A; 2067 C; 2260 G;
retroelement-containing vectors, cells and plants. Methoelement-containing vectors, cells and plants. Methoelements into cells
                                                                                                                                                                              Example
                                                                                                                                                                                                             characters to plants, especially
                                                                                                                                                                                                                                New nucleic acid molecules for imparting
                                                                                                                                                                                                                                                                 WPI; 2000-105586/09
                                                                                                                                                                                                                                                                                              Wright DA, Voytas DF
                                                                                                                                                                                                                                                                                                                              (WRIG/) WRIGHT (VOYT/) VOYTAS
                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroelement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean retroelement Calypso 2-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ35275;
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCCCCTTCTCGGGGA 18
                                                                                                                                                                              Page 107-111; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soybean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retrovirus;
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                                                                                                                                                                                                                                                                                                                                                                                98US-0087125
99US-0087125
                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US11858.
                                                                                                                                                                                                                                                                                                                                  y A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic plant; gene transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                 soybean
                                                                                                                                                                                                                      agronomically significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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             Methods are
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RESULT 4
AAZ35261
ID AAZ3
XX AAZ3
XX AAZ3
XX AAZ3
XX Rety
DT 27-1
CX Rety
KW Soylt
XX Solyc
OS ALAk
OS Piss
FT CDS
FT CDS
FT CDS
FT WY
FT CDS
PN W099
XX WPI
PF 28-1
XX WPI
DR P-P
XX WPI
DR P-P
XX WPI
DR P-P
XX WPI
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence selected from a retroelement primer binding site, envelope, gag, integrase, reverse transcriptase, protease or RNAse-H sequence (see AAZ35254-61). Also provided are plant retroviral particles that particles are used to transfer the nucleic acids into plant cells.
                                                          obtained from retrovirus-like elements (retroelements) calypso of soybean, cyclops of pea and athila of Arabidopsis thaliana. The invention provides molecular tools in the form of retroelements and
                                                                                                                                                                                                                                                                                                       (WRIG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retroelement; soybean; pea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid
               retroelement-containing vectors, cells and plants. Methods are provided for introducing the retroelements into cells, especially when the retroelement carries at least 1 agronomically-significant
                                                                                                                                            Claim 1(h); Page 84-88; 118pp; English.
                                                                                                                                                                          New nucleic acid molecules for imparting characters to plants, especially soybean
                                                                                                                                                                                                                            WPI; 2000-105586/09.
P-PSDB; AAY32434.
                                                                                                                                                                                                                                                                         Wright DA, Voytas DF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ35261;
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                                                                                                            The present sequence comprises a generic plant retroelement
                                                                                                                                                                                                                                                                                                                                                       29-MAY-1998;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09960842-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant generic retroelement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10482 BP; 3181 A; 1842 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               when the retroelement carries at least 1 agronomically-significant characteristic (ACS). In a preferred method, a helper cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sativum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                        WRIGHT
VOYTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCGCCGTTGTCGGGGA 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retrovirus; transgenic plant; Calypso; athila; cyclops; ss.
                                                                                                                                                                                                                                                                                                       DDA.
   (ACS).
                                                                                                                                                                                                                                                                                                                                                     98US-0087125
99US-0087125
                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US11858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 1482..6887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2297 G;
                                                                                                                                                                                          agronomically significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene transfer
a helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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γQ

TGGCGCCGTTGTCGGGGA 18

Query Match Best Local Matches

17; Conserv

Conservative

0;

Mismatches

Indels

0;

Gaps

0,

91.1%; 94.4%;

Score 16.4; Pred. No. 1.

.6e+02

DB

21;

Length

687;

Sequence

687

BP;

241 A; 135 C; 115 G; 196 T; 0 other;

selected

factors,

cytokines, antibodies, and growth factors. proteins such as hormones, enzymes,

interleukins,

clotting

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RESULT 5
AAF22107,
γQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                      18-MAR-1999;
01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2107/c
AAF22107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which expresses gag, pol and env sequences is used to enable transfer of a secondary construct which carries an ASC and has retroelement sequences that allow for replication and integration. Claimed isolated nucleic acid molecules comprise a nucleic acid sequence selected from a retroelement primer binding site.
                                           The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells expressing
                                                                                                                               Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors \mathbf{f} the construction of transgenic plant and animal cells -
                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Centromere; michrosome; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retroviral particles that are used to transfer the nucleic acids into plant cells.
                                                                                                          Claim 108; Page 274; 1449pp; English.
                                                                                                                                                                                                           Preuss D,
                                                                                                                                                                                                                                                                                                                                    17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                     WO200055325-A2.
                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12286 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             envelope,
                                                                                                                                                                                                                                  (UYCH-) UNIV CHICAGO.
                                                                                                                                                                                                                                                            17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1312
                                                                                                                                                                                  2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEGCECCETTETCEGEGA 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCGCCGTTGTCGGGGA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gag, integrase, reverse transcriptase, protease or equence (see AAZ35254-61). Also provided are plant
                                                                                                                                                                                                         Copenhaver
                                                                                                                                                                                                                                                                                                                                                                                                             thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana centromere conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                    2000WO-US07392
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                           ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ds.
                                                                                                                                                                                                           ζ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 3231 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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                                                                                  plant
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RESULT 7
AAF22303
ID AAF2
XX
AC AAF2
XX
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AAH51978/
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                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                       This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism.
                AAF22303;
                                                                                                                                                                                                                                                 Sequence 2364 BP;
                                           AAF22303 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 71-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drug target; growth; organism viability; characterisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis potential drug target gene SEQ
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12-NOV-1999;
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DB; AAG81127.
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                                                                                                                                                                                    17; Conserv
                                                                                                                                       TGGCGCCGTTGTCGGGGA 18
                                                                                                                        TGGCGCCGTTGTCGGAGA
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                                                                                                                                                                                     Conservative
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99US-0165124.
                                                                                                                                                                                                                                                 467 A; 775 C; 715 G; 407 T; 0 other;
                                             DNA;
                                                                                                                                                                                                  91.1%;
94.4%;
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                                              611590
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                                                                                                                                                                                                  Score 16.4; DB 22; Pred. No. 1.6e+02;
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RESULT 8
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Best Local
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                              Mycobacterium tuberculosis; strain H37Rv; strain CDC variation; epidemiology; patient treatment; epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                    the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clott factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors in the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                24-JUN-1998;
                                                                                                       Mycobacterium
                                                                                                                                                                                                                                         AAI99683 standard; DNA; 4403765 BP
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 611590 BP; 181893 A; 124460 C; 120254 G; 184983 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 45;
         24-JUN-1998;
                                                        25-SEP-2001.
                                                                                                                                                                  Mycobacterium tuberculosis strain H37Rv genome
                                                                                                                                                                                         15-JAN-2002
                                                                                                                                                                                                                 AAI99683
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17; Conserv
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                                                                                                        tuberculosis
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99US-0134770.
99US-0153584.
           98US-0103840
                                 98US-0103840
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Pred. No. 1.
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RESULT 9
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium
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                                           determining the nucleotide genome corresponding to pos
                                                                                                                                                                                                                                                                                                    Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification, but was obtained in electronic format
at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
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                                                                                                                                                                                                                                                                                                                                variation;
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                             H37Rv differ
                                        strain variation of Mycobacterium tuberculosis, g the nucleotide sequence of the strain at positi responding to positions where M. tuberculosis str
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                                                                                                                                                                                                                                                                                                                                                                          tuberculosis
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Pred. No. 1.1e+02;
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Claim 4; SEQ

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Sequence Listing; English

sequence data

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RESULT 1
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                                                                The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
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                                                                                                                                                                                                       Evaluating strain variation of Mycobacterium tuberculosis, competermining the nucleotide sequence of the strain at positions genome corresponding to positions where M. tuberculosis strains
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              monitoring
                          tuberculosis
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variation; epidemiology; patient treatment;
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                                        H37Rv (AAI99682). The method is useful for evaluating strain variation M. tuberculosis and has valuable application in the fields of
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Pred. No. 1.1e
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                             treatment
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RESULT 11
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                                                                                                                                                                                                             The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199683). The method is useful for evaluating strain variation c M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID-6294328B1.
                                                                                                                      Sequence 4411529 BP;
                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and \rm H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-647261/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis; strain H37Rv; svariation; epidemiology; patient treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
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                                                                                                                                                                                                 monitoring.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1998;
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17; Conser
                                                           l Similarity
17; Conserv
TGGCGCCGTTGTCGGAGA
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                            TGGCGCCGTTGTCGGGGA 18
                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain H37Rv; strain CDC
                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser CM,
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Pred. No. 1
                                                                        Score 16.4; DB 23
Pred. No. 1.1e+02
                                                           Mismatches
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                                                                                        DB 22;
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                                                                                        Length 4411529;
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monitoring; d
                                                                                                                      758379 T; 0 other;
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RESULT 12
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Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; drug; side effect; cancer; central nervous system; cardiov gastrointestinal; respiratory system; single nucleotide pc SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek
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05-SEP-2000; 2000DE-1044543.
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207
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                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                       BP; 49
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                                                                                                                                                                                                                                                                                                                                       A; 63 C; 174 G;
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                                                                                                                                                                                                            85.6%; Score 15.4;
94.1%; Pred. No. 4.
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RESULT 14
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                                                                                                                                                                                                                                 This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one commended and the degree of hybridisetion to both classes is determined from the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABD13410-ABD54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                   Matches
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              AAF08402 standard; cDNA; 778 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A,
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05-SEP-2000;
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                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis and.
                                                                                         303
                                                                                                                   2 GGCGCCGTTGTCGGGGA 18
                                                                                                                                                               Similarity
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                                                                                                                                                                                                              509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ng the degree of cytosine methylation in genomic DNA, useful osis and prognosis, comprises selective hybridization of from chemically treated DNA
                                                                                                                                                   Conservative
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2000DE-1044543
                                                                                                                                                               85.6%;
94.1%;
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                                                                                                                                                                                                           C; 63
                                                                                                                                                               Score 15.4;
Pred. No. 4
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em; single nucleotide polymorphism;
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                                                                                                                                                               4:8e+02;
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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the case genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production optential of the microorganisms to be improved. New genes may be cell discovered, possible functions of unknown open reading frames can be compined and gene copy number variation and stability can be constituted and gene copy number variation and stability can be reproved to changes in culture conditions, environmental stress, spore adapt to changes in culture conditions, environmental stress, spore the continuous files of the second continuous conti
                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF1147 represents ESTs from Aspergillus Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF11874 to AAF11878 represents ESTs from Aspergillus oryzae; and AAF1879 to AAF15337 represents ESTs from Trichoderma reesei, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 86; Page 737; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
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                                                                                                                                                                                                                                                                                                                                           Sequence
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94.1%;
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Pred. No. 4.7e+02
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RESULT 15 ABK87940

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ABK87940 standard; cDNA; 1649 BP

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CC The invention discloses an isolated 25206 polypeptide, a human CC short-chain dehydrogenase/reductase (SDR) family member. Members of this CC family catalyse the reversible, rate limiting conversion of retinol to CC retinal. Retinal is then converted to retinolc acid which plays a key CC role in the regulation of embryoric development, spermatogenesis and CC epithelial differentiation. Short chain dehydrogenases are important in CC the metabolism of small molecules, production/removal of biologically CC important molecules that modulate development and growth, elimination of CC conditions. The polynuclectide and polypeptide are useful for identifying CC compounds which binds to them, for identifying compounds which binds to them, for identifying compounds which binds to them, for identifying compounds which modulate CC the activity of the polypeptide in a sample, for modulating aberrant activity of the polypeptide in a sample, for modulating aberrant activity of £ 25206 expressing cells (e.g. a cancerous, pre-cancerous or neural CC call) and for treating or preventing disorders characterised by the aberrant activity. The 25206 molecules can act as diagnostic targets and CC therapeutic agents for controlling one or more cellular proliferative, CC cancer, tumours, carcinoma, sarcoma and Hodgkin's disease, parkinsonism CC cancer, tumours, carcinoma, sarcoma and Hodgkin's disease, Parkinsonism CC cancer, carcinoma, sarcoma and Hodgkin's disease, Parkinsonism CC cancer, carcinoma, sarcoma and modulation disease, Parkinsonism CC cancer set the disorders (e.g. cancer set the disorders (e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated 25206 polypeptide, a human short-chain dehydrogenase/reductase family member, useful as diagnostic targets and therapeutic agents for treating cancer, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene; ss; cytostatic; nootropic; neuroprotective; antitumour; 25206; short-chain dehydrogenase; short-chain reductase; SDR; retinol; retinal; retinolacid; embryonic development; spermatogenesis; epithelial differentiation; metabolism; development; growth; proliferative disorder; hammatopoletic disorder; cancer; tumour; afforderitive disorder; hammatopoletic disorder; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differentiative disorder; carcinoma; sarcoma; Hodgkin's disease; neurodegenerative disorder; Alzheimer's disease; Parkinsonism; progressive supranuclear palsy; reproductive disorder; ovarian tumours;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 101-102; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-547697/58.
P-PSDB; AAU99344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polycystic ovarian disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macbeth KJ;
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Sequence 1649

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275 A; 543 C; 532 G; 299 T; 0 other;

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Matches 16;
1274 GGCGCCTTTGTCGGGGA 1290
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16; Conserv
         2 GGCGCCGTTGTCGGGGA 18
                                    Conservative
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94.1%;
                                  Score 15.4; DB 24;
Pred. No. 4.6e+02;
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Search completed: June 20, 2003, 21:58:31 Job time: 22.3019 secs

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Result
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12-478-39 ICE 39, Application No. 6331662 INO. 6331662 INO. 6331662 CANT: Wright, Day COANT: Voytas, Day OF INVENTION: PREFERENCE: P-106 INT APPLICATION NO INT FILING DATE: ER APPLICATION NO ER FILING DATE: R OF SEQ ID NOS: R OF SEQ ID NOS: NO 39 TH: 27 IDNA NISM: Glycine ma. NISM: Glycine ma.	ilarity Conser GCGCCGT	478-2 2, Application 0, 6331662 INFORMATION: NT: Wright, Dav NT: Woytas, Dan F INVERS: P-1065 FERENCE: P-1065 APPLICATION NU FILING DATE: 11 APPLICATION NU		7
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RESULT 5
US-09-322-478-17
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EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 9829
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Patent No. 6331662
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Patent No. 6331
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APPLICANT: W19ht, David A.
APPLICANT: W19ht, David A.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087125
EARLIER APPLICATION NUMBER: 65/087125
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
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APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
CURRENT FILING DATE: 1999-05-28
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APPLICANT: FLEISCHMAN, Robert
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APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DIA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
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OTHER INFORMATION: represent
                                                                                                                                                                                                            TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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RESULT 7
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; Patent No. 6294328

APPLICANT: FLEISCHMAN, Robert APPLICANT: WHITE, Owen R.

WHITE, Owen R. FRASER, Claire M.

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APPLICANT:
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APPLICANY: FRASE, Claire M.
APPLICANY: FRASE, Claire M.
APPLICANY: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
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CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                  APPLICANT: FLEISCHMAN, Robert D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLEISCHMAN, Robert D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: MYCObacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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APPLICATION NUMBER: US/09/103,840A
FILING DATE: 1998-06-24
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94.48;
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Pred. No. 1
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Pred. No. 1
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; NAME/KEY: unsure
; LOCATION: (1012)
US-09-452-239-35
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SEQ ID NO 35
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Best Local (
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Best Local :
                                     Matches
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EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: BB1284 US NA
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TYPE: DNA
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TYPE: DNA
ORGANISM: Triticum
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17; Conserv
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1 TGGCGCCGTTGTCGGGGA
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16; Conserv
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(874)
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(970)..(971)
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                                     Conservative
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                                                82.2%;
88.9%;
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Pred. No. 1
                                                Score 14.8;
Pred. No. 1.
                                    Mismatches
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                                                             DB 4;
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RESULT 11
US-09-452-239-41/c
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LENGTH: 1078
TYPE: DNA
ORGANISM: Triticum aestivum
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APPLICANT: Fader, Gary M.
APPLICANT: Fader, Gary M.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-Coa O-Methyltransferase
FILE REFERENCE: BB1284 US M.
CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Meiji Seika Kaisha, Ltd.
APPLICANT: Moriya, Tatsuki
TITLE OF INVENTION: Systems for the Mass Production of Proteins
TITLE OF INVENTION: of the Genus Humicola
FILE REFERENCE: VX990054
CURRENT APPLICATION NUMBER: US/09/230,225B
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 34
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EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
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                                                                                                                                          LOCATION: (536)..(1029)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (458)..(477)
OTHER INFORMATION:
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                                                                              NAME/KEY: Intron
LOCATION: (1030)..(1141)
                                                                                                                                                                                                                                                          NAME/KEY: Intron
LOCATION: (478)..(535)
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                                                         OTHER INFORMATION:
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Local Similarity 88.9%;
les 16; Conservative
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(1142)..(1761)
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Pred. No. 1.5e+02;
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; SEQ ID NO 94
; LENGTH: 3348
; TYPE: DNA
; ORCANISM: Candida tropicalis
US-09-302-620B-94
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US-09-302-620B-94
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; LCATION: (1643)..(1648)
; OTHER INFORMATION: Cleavage siteStuI
US-09-230-225B-3
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Best Local Similarity 80...
The state of the 
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                                                                                                                                       Query Match
Best Local
                                                                                                                  Matches
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APPLICANT: Craft, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIOCREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
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LOCATION: (1505)..(1510)
OTHER INFORMATION: Cleavage site BglII
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LOCATION: (1253)..(1259)
OTHER INFORMATION: Cleavage site BamHl
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LOCATION: (688)..(693)
OTHER INFORMATION: Cleavage site SmaI
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1228 TGGCGCCGTTGTTGGCGA 1211
1140 TTGCGCCGTTGTTGGGGA 1157
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                                                                                                                  16;
                                                         1 TGGCGCCGTTGTCGGGGA 18
                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cornett, Cathy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madduri, Krishna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eirich, Dud.
Eshoo, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loper, John C.
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..(2044)
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88.9%;
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88.9%;
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                                                                                                            Score 14.8; DB 4;
Pred. No. 1.4e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 4;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                           DB 4;
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                                                                                                                                                                        Length 3348;
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-09-199-637A-111

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; SEQ ID NO 111
; LENGTH: .6909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-611-757-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Datent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/199,637A: CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TSONGALIS, JOHN
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,985
FILING DATE: 20-MAY-1994
APPLICATION NUMBER: US 025,396
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhang-Keck, Zhen-Yang
APPLICANT: Young, LaVonne
TITLE OF INVENTION: No. 5859230-A/No. 5859230-B/No. 5859230-C/No. 5859230-D/No. 51
TITLE OF INVENTION: Agents and Molecular Cloning Thereof
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                         FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dehlinger & Massuccite 250 STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2627 TGGCGCCGTTGCCGGGCA 2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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5859230
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                                                                                                                                                                                                                                                                                      CA
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Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drenkard, Eliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tan, Man-Wah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ausubel,
                                                                                                                                                                                                                                                                  USA
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Wages, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim, Jungsuh P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00786/361002
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                                                                                                                us/08/611,757
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Pred. No. 1.4e
0; Mismatches
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                                                                                                ; INDIVIDUAL ISOLATE: GB Clone 475-12-3 US-08-611-757-14
                                                  Matches
                                                              Query Match
Best Local (
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 231 base pairs
                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                      MOLECULE N
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
07/922,493
                                                                                                                                                   MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
131 GCGCCGTTGTCGGTGA 146
              3 GCGCCGTTGTCGGGGA 18
                                                              Similarity
                                                                                                                                                                                                nucleic acid
                                                 Conservative
                                                                                                                                                                           linear
                                                                                                                                                                                       double
                                                                                                                                                                                                                                                                                                                 Gary R.
                                                                                                                                                                                                                                                                 324-0880
                                                             80.0%;
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                                                  0;
                                                              Score 14.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                          4600-0201
                                                 Mismatches
                                                              2.3e+02;
                                                                        DB 2;
                                                                        Length 231;
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Gaps

0,

Search completed: June 20, 2003, 23:25:44 Job time: 14.1792 secs

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Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB seq
  Published_Applications_Na:*

1: /cgn2_6/ptodata/2/pubpna/U
2: /cgn2_6/ptodata/2/pubpna/U
3: /cgn2_6/ptodata/2/pubpna/U
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6: /cgn2_6/ptodata/2/pubpna/U
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13: /cgn2_6/ptodata/2/pubpna/U
14: /cgn2_6/ptodata/2/pubpna/U
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-965-553-2
18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tggcgccgttgtcgggga 18
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
:: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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3971.420 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	10	US-09-965-553-2	Sequence 2, Appli
2	18	100.0	27	10	US-09-965-553-39	39
ω	18	100.0	9829	10	US-09-965-553-19	19,
4	18	100.0	10482	10	US-09-965-553-23	•
5	18	100.0	12286	10	US-09-965-553-17	17,
6	16.4	91.1	2000	9	US-09-938-842A-5131	Sequence 5131, Ap
c 7	16.4	91.1	2364	9	US-09-712-363-32	₽.
c 8	15.4	85.6	251	10	US-09-878-574-10644	Sequence 10644, A
c 9	15.4	85.6	262	10	US-09-878-574-12308	Sequence 12308, A
c 10	15.4	85.6	269	10	US-09-878-574-12035	Sequence 12035, A
c 11	15.4	85.6	269	10	US-09-878-574-13422	Sequence 13422, A
c 12	15.4	85.6	272	10	US-09-878-574-11753	Sequence 11753, A
c 13	15.4		273	10	US-09-878-574-15624	Sequence 15624, A
C 14	15.4	85.6	275	10	US-09-878-574-12670	Sequence 12670, A
c 15	15.4	85.6	275	10	US-,09-878-574-14365	Sequence 14365, A
c 16	15.4	85.6	276	10	US-09-878-574-8192	Sequence 8192, Ap
c 17	15.4	85.6	285	10	US-09-878-574-12806	Sequence 12806, A
18	15.4	85.6	449	9	US-09-918-995-28499	N
19	15.4	85.6	1649	9	US-09-997-816-1	Sequence 1, Appli

a	a	a	O	o	a	O	a									a	C	a	a	c	c		a	c
45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.8	14.8	٠	14.8	14.8	14.8	14.8	٠	14.8	14.8	14.8	•	14.8	٠	14.8	14.8	14.8
80.0	80.0	80.0	80.0	80.0	80.0							82.2												
342	334	303	271	269	264	249	189	3309400	6909	3348	3348	3348	3348	3348	1215	1113	1110	1110	1078	1018	944	561	496	254
10	10	10	10	10	10	10	10	و	9	9	9	9	9	9	9	ø	9	9	10	10	10	10	9	10
US-09-878-574-2125	US-09-878-574-688	US-09-878-574-15351	US-09-878-574-14193	US-09-878-574-10867	us-09-878-574-15236	US-09-878-574-15547	US-09-821-167-8	US-09-738-626-1	US-09-975-719-111	US-09-976-800-94	US-10-138-916-94	US-10-138-905-94	US-10-139-031-94	US-10-138-838-94	US-09-738-626-1258	5	US-10-121-988-145	US-10-121-988-79	US-09-452-239-41	US-09-452-239-35	US-09-974-300-5723	US-09-864-761-9555	US-09-918-995-401	US-09-923-876-1817
Sequence 2125, Ap	Sequence 688, App	Sequence 15351, A	Sequence 14193, A	Sequence 10867, A	Sequence 15236, A	Sequence 15547, A	Sequence 8, Appli		Sequence 111, App	Sequence 94, Appl	Sequence 1258, Ap	Sequence 82, Appl	Sequence 145, App	Sequence 79, Appl	Sequence 41, Appl	Sequence 35, Appl	Sequence 5723, Ap	Sequence 9555, Ap	Sequence 401, App	Sequence 1817, Ap				

ALIGNMENTS

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                                                                                                                                                       RESULT 2
US-09-965-553-39
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Whiches 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-965-553-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-965-553-2
GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NO
SOFTWARE: PatentIn
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel
                                                                                                                 Sequence 39, Application US/09965553 Patent No. US20020112259A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09965553 Patent No. US20020112259A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VOYtas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: p-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322/478
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
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Pred. No. 5
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Sequence 23, Application US/0996553

Patent No. US2002011259A1

GENERAL INFORMATION:
APPLICANT: Wright, David A.
APPLICANT: Wright, David A.
APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/965,553

CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
SEQ ID NO 39
LENGTH: 27
TYPE: DNA
ORGANISM: Glycine max
US-09-965-553-39
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US-09-965-553-19
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GENERAL INFORMATION:

APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
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Best Local Similarity
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SEQ ID NO 19
LENGTH: 9829
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PRIOR ETILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087125
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
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PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
                                     SOFTWARE:
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CURRENT FILING DATE: 2001-09-27
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PRIOR APPLICATION NUMBER: 09/322
PRIOR FILING DATE: 1999-05-28
LENGTH: 10482
                    ID NO
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                                  PatentIn Ver
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20020112259A1
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Pred. No. 3
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; OTHER INFORMATION: Description of Artificial Sequence: plant ; OTHER INFORMATION: retroelement sequence US-09-965-553-17
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                                   NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 5131
LENGTH: 2000
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Best Local Similarity
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Best Local Similarity 100
Matches 18; Conservative
                                                                                                  PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                            TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                           APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR FILING DATE: 1998-05-29
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CURRENT FILING DATE: 2001-09-27
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APPLICANT: Voyta
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TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
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ORGANISM: Arabidopsis thaliana
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Pred. No. 3
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Pred. No.
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                                                                                                                                Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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SEQ ID NO 32
LENGTH: 2364
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              APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT PILING DATE: 2001-12-21
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APPLICANT: MATCOTTE, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR EILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
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PRIOR FILING DATE: 2000-01-28
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PRIOR APPLICATION NUMBER: 09/333,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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APPLICATION NUMBER: 60/134,093
FILING DATE: 1999-05-14
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5. US20020164588A1
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17; Conser
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Pred. No. 23;
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Pred. No. 2
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                                                                                  Other
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PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEO ID NO 12308

LENGTH: 262

TYPE: DNA

ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701065609H1
US-09-878-574-12308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 251

: TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: 700967905H1

US-09-878-574-10644
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US-09-878-574-12035/c
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NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 10644
                                                                     SEQ ID NO 12035
LENGTH: 269
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                                                                                                                                                                                                                                                                                                                                Sequence 12035, Application US/09878574 Patent No. US20020110548A1
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Best Local
                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(15401)B CUFRENT APPLICATION NUMBER: US/09/878,574 CURRENT FILING DATE: 2001-12-21 PRIOR APPLICATION NUMBER: 09/333,535 PRIOR FILING DATE: 1999-06-14 NUMBER OF SEQ ID NOS: 15775
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TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone
-09-878-574-12035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                             APPLICANT: Byrum, Joseph R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
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nes 16; Conserv
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                                                                                                                                                                                                                                                                                                               INFORMATION:
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Thompson, Michael D
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94.1%;
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                 ID: 701065234H1
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0; Mismatches
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Pred. No. 8
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: U9/33,535
PRIOR FILING DATE: 1999-06-14
INUMBER OF SEQ ID NOS: 15775
SEQ ID NO 13422
LENGTH: 269
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701067081H1
US-09-878-574-13422
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US-09-878-574-13422/c
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US-09-878-574-11753/c
; Sequence 11753, Application US/09878574
; Patent No. US20020110548A1
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701054849H1
US-09-878-574-11753
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 11753
LENGTH: 272
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Best Local Similarity
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                                                                             Similarity
GGCGCCGTTGTCGGTGA 210
                            GGCGCCGTTGTCGGGGA 18
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                                                                Conservative
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94.1%;
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Pred. No. 8
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Pred. No. 8
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Pred. No. 8
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Matches
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Oth
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)8
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO 12670
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID:
US-09-878-574-12670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID:
US-09-878-574-15624
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US-09-878-574-15624/c
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                                                                                          US-09-878-574-14365/c

; Sequence 14365, Application US/09878574

; Patent No. US20020110548A1
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SEQ ID NO 15624
LENGTH: 273
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APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
                                                                          GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic acid Molecules and Other Molecules Associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15775
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Local Similarity 94.1%;
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94.1%;
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Pred. No. 8
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Pred. No. 8
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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110: c
111: c
112: c
113: d
114: d
115: d
116: d
117: d
118: d
119: d
120: d
121: d
122: d
123: d
123: d
123: d
124: d
125: d
126: d
127: d
128: d
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BH6808149 BH725980 BI642756 BH552125 BH445346 BH424623 AZ922191 CNSO0XJK BH436253 BH744134 BH705588 BH7145888 BH7145888 BH51796667 BH727785 вн590633 BG299448
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BOGU171-TR
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ALIGNMENTS

FEATURES source										COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AQ288973/c	
e 1250	High quality sequence stop: 117.	Class: BAC ends	Seg primer: TAATACGACTCACTATAGGG	Email: rwing@clemson.edu	Fax: 864 656 4293	Tel: 864 656 7288	100 Jordan Hall, Clemson, SC 29634, USA	Clemson University	Clemson University Genomics Institute	Contact: Wing RA	Unpublished (1998)	A BAC End Sequencing Framework to Sequence the Rice Genome	Wing, R.A. and Dean, R.A.	1 (bases 1 to 250)	Ehrhartoideae; Oryzeae; Oryza.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Oryza sativa	Oryza sativa.	GSS.	AQ288973.1 GI:3950419	AQ288973	nbxb0033H14f, DNA sequence.	ary Oryza sa	AQ288973 250 bp DNA linear GSS 03-DEC-1998		

/clone="nbxb0033H14f"

/cultivar="Nipponbare" organism-"Oryza sativa"

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RESULT 2
BH731480
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Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 552)

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Town, G.D., Parken, S., Utterback, T. and Fraser, C.M.
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                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BH731480
                                                                                                                                                                                               Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                 Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica oleracea.
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    HindIII; Rice is one of two most popular grains in the
    world. Half of the world population especially those
    inhabiting highly populated areas of the humid tropics
    and subtropics, rely on rice as their primary source of
    carbohydrate. Monocotyledonous rice is a diploid plant
    (2n=24) with a haploid genome equivalent of 431 Mbp
    (Arumuganathan and Earle, 1991). The relatively small
    genome of rice, three times larger than that of
    Arabidopsis, makes it suitable for genomic studies. In
    order to facilitate positional cloning, physical mapping
    and genome sequencing of rice, we have constructed a BAC
    library from Oryza sativa, Nipponbare variety. The
    library contains 36,864 clones with an average insert size
    of 128.5 Kb providing 10.9 haploid genome equivalents. The
    deep coverage allows the isolation a particular sequence
    with a probability of 99.9 % Two high density filters,
    each containing 18,432 clones (doubly spotted), represent
    the whole library for colony screening."
                                                                                                                                                  sheared ends.
/db_xref="taxon:3712"
/clone="BOHZO16"
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/tissue_type="Leaf"
/lab_host="E. coli DH10B"
                                               /organism="Brassica oleracea"
/strain="TO1000DH3"
                                                                                                                      Location/Qualifiers
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Brassica oleracea.
Brassica oleracea
Eukaryota; Viridip
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Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris Town
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                                                                                                                                                                                                                                                                                                           /clone_lib="BOGC"
/note="Vector: pHOS1; Site_1: Bs
/note="Vector: pHOS1; Site_1: Bs
genomic DNA inserted into pHOS1
genomic 201 t 109 g 201 t
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1. .624
                                                                                                BOGD
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/strain="TO1000H3"
/db_xref="taxon:3712"
/clone="BOGCW07"
 Viridiplantae;
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Pred. No. 2.5e+02;
; Mismatches 0;
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Pred. No. 2.6e+02;
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BH214458
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BH214458
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Other_GSSs: BOGDG03TF
                                  see as an authority for the mapping/naming: Cregan P.B., T. Jarv. A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. Varroai, D.G. Lohnes, J. Chung, and J.E.Specht. 199a. An integrated genetic linkage map of the soybean genome. Crop Sci. 39:1464-1490.
                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Shoemaker Randy C
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18; Conser
Seq primer: M13F
Class: BAC ends.
                                                                                                                                                                                                                                                                           Agronomy Department
Iowa State Universi
                                                                                                                                                                                                                                                                                                                                                   Marek, L.F., Paz, M., Darnielle, L.,
BAC End sequences from a soybean
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DNA is from a doubled haploid provided
                                                                                                                                http://genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase.
                                                                                                                                                                       Email: rcsshoe@iastate.edu
This BAC identified by SSR Satt077.For more information, see
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S, IA 50011-1010, USA
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/Clone_lib="BGGD"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
146 c 144 g 192 t
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/clone="BOGDG03"
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1. .668
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/strain="TO1000DH3"
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. 2.7e+02;
ches 0;
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genomic library (ISU)
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RESULT 6
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BH484542
 18;
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                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                              Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOGWE45TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
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Brassica oleracea
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BOGWE45TF BOGW Brassica
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                                                                             /Clone_lib="BOGW"
/Clone_lib="BOGW"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared /note="Vector: pHOS1 using BstXI linkers" genomic DNA inserted into pHOS1 using BstXI linkers" 139 c 140 g 180 t
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/tissue_type="cotyledon leaves"
/dev_stage="cotyledon"
                                                                                                                                                                                                     /organism="Brassica oleracea"
/strain="TO1000DH3"
                                                                                                                                                                /db_xref="taxon:3712"
/clone="BOGWE45"
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/db_xref="taxon:3847"
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Score 18; DE
Pred. No. 2.7
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Pred. No. 2.7e+02;
; Mismatches 0;
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DB 17;
2.7e+02;
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RESULT 7
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BOMMT13TR BO_2_3_KB Brassica
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Other_GSSs: BOMMT13TF
Contact: Chris Town
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Robinia pseudoacacia.

Robinia pseudoacacia

Robinia pseudoacacia

Robinia pseudoacacia

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Fabaceae; Papillonoideae; Robinieae;

Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Robinieae;
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Han,K.-H., Yang,J., Park,S., Paule,C.R., Kapur,V., Kamdem,D.P. and Keathley,D.E.
Analysis of gene expression patterns in trunk wood black locust (Robinia pseudoacacia)
                                                                                                                                                                                                                                                         BI642756
TZS973 TZS (Sapwood-heartwood transition zone of black Summer) Robinia pseudoacacia cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
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                                                                                           Robinia
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                                                                        (bases 1 to 697)
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301-838-0208
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llarity 100.0%;
Conservative
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/clone="BOMMT13"
/clone="BOMMT13"
/clone=1b="BO_2_3_KB"
/clone=1b="BO_2_3_KB"
/clone=1b="BO_2_3_KB"
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
a 182 c 139 g 185 t
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1. .694
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/strain-"TO1000DH3"
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Pred. No.
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2.7e+02;
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                           of a mature
                                                                Retzel, E.F.,
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COMMENT
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AUTHORS
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BH552125
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Query Match
Best Local Similarity
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Contact: Kyung-Hwan Han
Department of Forestry
Michigan State University
126 Natural Resources, East Lansing, MI 48824-1222,
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BH552125
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BOHES25TF BOHE Brassica
                                                                                                                                                                                                                                                                                                                           Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHES25TR
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вн552125.1
                                                                                                                                                                                                           Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TF
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                                                                                                                                                                                                                                                        9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                  Class: sheared ends.
                                                                                                                                                                                                                                                                                                               Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCGCCGTTGTCGGGGA
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517 432 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / unce="Vector: lambda TriplEx; Site_1: Sfi IA; Site_2: Sfi IB; The cDNA library was made from the sapwood-heartwood transition zone of a mature black locust tree collected in Michigan in late July."

Michigan in late July."

Michigan in late July."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Robinia pseudoacacia"
/db_xref="taxon:35938"
/clone_lib="TZS (Sapwood-heartwood transition zone black locust - Summer)"
                                                                                                              /organism="Brassica Ole
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHES25"
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                                                       /note="Vector: pHOS1; Site_1: BstXI; genomic DNA inserted into pHOS1 using 181 c 138 g 198 t
                                                                                                                                                                       Location/Qualifiers
1. .708
                                                                                                 /clone_lib="BOHE"
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     Score 18;
Pred. No.
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2.7e+02;
       ; DB 17;
. 2.7e+02;
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                    Length 708
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g BstXI linkers"
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BOHES25, DNA
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RESULT 11
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AUTHORS
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AUTHORS
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ORGANISM
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                                                                                                                                       Brassica oleracea.
Brassica oleracea
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BOGEE39TR BOGE Brassica
                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Tel: 301-838-3523
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOHNP83TF
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GSS.
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BOHNP83TR BOHN Brassica
                                                      1 (bases 1 to 722)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                   Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
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is from a doubled haploid
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/note="Vector: pHOS1; Site_1: Bstx1; 2-3 kb
genomic DNA insertted into pHOS1 using BstXI
179 c 135 g 202 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHNP83"
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Pred. No. 2.7e+02;
Pred. No. 2.7e+02;
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                                                                                                                                                                    cus. Please see as an authority for the mapping/naming: Cregan P.B., T. Jarvik, A.L. ush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. VanToai, D.G. Lohnes, J. Chung, and J.E. Specht. 1999a. An integrated genetic linkage map of the soybean genome. Crop Sci. 39:1464-1490
                                                                                                                                                                                                                                                                                                                                                                                                          Larsen,D., Mudge,J., De
BAC end sequences from
Unpublished (2001)
Contact: Young Nevin D
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                                                                                                                                        Seq primer: M13F
Class: BAC ends.
                                                                                                                                                                                                                                                       Sequence on contig Gm_A455_ctg_a near unmapped duplicate of pA455.
For more information, see SoyBase at:
http://genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase&class=Lo
                                                                                                                                                                                                                                                                                                                           Tel: 612 625 2225
Fax: 612 625 9728
                                                                                                                                                                                                                                                                                                                                                            495 Borlaug Hall, 1991 Upper Buford Circle,
                                                                                                                                                                                                                                                                                                                                                                           Department of Plant Pathology University of Minnesota
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DNA is from a doubled haploid
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                           Email: neviny@tc.umn.edu
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/clone_lib="BOGE"
/clone_lib="BOGE"
/clone_lib="BOGE"
/clone_lib="BOGE"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1, Site_1: BstXI linkers"
genomic DNA inserted into pHOS1 using BstXI linkers"
a 132 c 110 g 226 t
/db_xref="taxon:3847"
/clone_lib="UMN Soybean BAC Library (pECSBAC4 EcoRI)
Glycine max genomic clone"
/tissue_type="cotyledon leaves"
                                                                                                                       Location/Qualifiers
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/strain="TO1000DH3"
                                                                      /cultivar="Faribault"
                                                                                       /organism="Glycine max"
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2.7e+02;
les 0;
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RESULT 13
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 747)

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOGDT64TF
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BOGDT64TR BOGD
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DNA is from a doubled haploid
Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-3523
Fax: 301-838-0208
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 BH590633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chris Town
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genomic DNA inserted into pHOS1 using BstXI linkers"
188 c 136 g 209 t
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                                                                                                                                                                                                                                                                          /organism-"Brassica oleracea"
/strain-"701000DH3"
/db_xref-"taxon:3712"
/clone-"BGGDT64"
/clone_11b-"BOGD"
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Other_GSSs: BOHBZ5ZTR
Contact: Chris Town
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1 (bases 1 to 768)

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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DNA is from a doubled haploid
                                                                           9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                            BOGWY06TR BOGW Brassica oleracea genomic clone
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                Class: sheared ends
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                                            DNA is from a doubled
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                                                           cdtown@tigr.org
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                                                                                                                                           Chris Town
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/clone="BOHBZ52"
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/strain="TO1000DH3"
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thes 0;
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BASE COUNT ORIGIN δÃ Search completed: June 20, 2003, 22:39:16 Job time: 73.1132 secs В Query Match 100.0%; Score 18; DB 17; Length 770; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 18; Conservative 0; Mismatches 0; Indels source 1. .770
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genomic DNA inserted into pHOS1 using BstXI linkers"
220 a 130 c 167 g 253 t 0; Gaps 0;

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